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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                    No.
        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
              430.5

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                                                                                                                                                 2024
                                                                                                                                                                Match Length DB
                                                                                                                                                                                                                                                                                           Query
     671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                    SPTREMBL 21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                       Q98998
                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (without alignments)
881.793 Million cell updates/sec
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                                                                                 075963 homo sapien
09mzu2 oryctolagus
09mzu3 oryctolagus
09mzu3 oryctolagus
096re8 homo sapien
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                   Q9ud67
096716
                                                       Q13729
Q13675
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                                   Q98998 xenopus lae
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3 oryctolagus
8 homo sapien
1 homo sapien
9 homo sapien
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pan troglod
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ALIGNMENTS

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## RESULT 1 Q96P66 Query Match Best Local Matches 397; Conservative genome sequence."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF411115; AAL26486.1; -. EMBL; AB083588; BAB89301.1; -. InterPro; IPR000276; GPCR\_Rhodpsn. Pfam; PF00001; 7tm 1; 1. PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1 1; UNKNOWN 1. PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1. Receptor. SEQUENCE 096P66; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) G protein-coupled receptor (Putative G-protein coupled receptor). Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S., "Identification of G protein-coupled receptor genes from the human SEQUENCE FROM N.A. MEDLINE=21458557; PubMed=11574155; Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O., Lewis T., Evans J.F., George S.R., O'Dowd B.F.; SEQUENCE FROM N.A. Gene 275:83-91(2001). genes "Discovery and mapping of ten novel G protein-coupled receptor Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; Homo sapiens (Human) Q96P66 Similarity 508 AA; PRELIMINARY; 56716 MW; E20A409F65C95BB5 CRC64; 96.7%; Score 2024; DB 4; Length 508; 78.1%; Pred. No. 7.6e-179; tive 1; Mismatches 0; Indels 110 PRT; 508 AA

Indels 110; Gaps

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                                                              Matches
                                                                           Query Match
Best Local :
                                                                                                                         Receptor.
SECUENCE
                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q90X46
                                                                                                                                                   Pfam; PF000001; 7tm_1; 1. FROSTTE, PS00237; G_FROTEIN_RECEP_F1_1; UNKNOWN_PPOSTTE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                               Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AL590146; CAC94897.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             SC: BZ2015 4
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NGTAVANSTNGLDDNGLM------VLEŚVSIIIIAILACLGNLVIVVTLYKKPYLLTPS 58
                           NSTPESNSSHTCMPLSKMPISLAHGIIPSTVLVIFLAASFVGNIVLALVLQPKPQLLQVT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480
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                                                                                                                                                                                                                                                                                                 TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVENEDEEGAEKKEEFQDE
                                                            101;
                                                                            Similarity
                                                                                                                         402 AA;
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     (TYEMBLrel. 19, Created)
(TYEMBLrel. 19, Last sequence update)
(TYEMBLrel. 20, Last annotation update)
(novel protein similar to human G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV
                                                                                                                         44373 MW; 5FB8875874267F00 CRC64;
                                                                      20 6%; Score 430 5; DB 13; Length 27.9%; Pred. No. 1.3e-31;
                                                          78; Mismatches 138; Indels
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Best Local :
                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a novel human G-protein coupled receptor.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF091890; AAC61598.1;
Interpro; IPR000276; GPCR_Rhodpsn.
Ffam; pF00001, 7tm.1, 1.
PPOSITE; PS00237; G PPOTEIN RECEP F1 1; UNKNOWN 1
PPOSITE; PS00237; G PPOTEIN RECEP_F1 2; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-protein coupled receptor RE2.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           075963;
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 269
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SRENS-----NSNPPLPECYQCKAAKVIFIIIFSYVLSLGPY-CFLAVLAVW--VDVET 319
                                                                         IACYSVVFCAARROHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDEMNIPESLPP 268
                                                                                                                                                 YLLLYGTWIVAILQSTEPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVIPLIVM 208
                                                                                                                                                                                       VTSSIEREWIFGVVWCNFSALLYLLISSASMLTIGVIAIDFYYAVLYFMVYFMYITGNPA 144
                                                                                                                                                                                                                                                                     GVIITQFIAIIVITIFVCLGNLVIVVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQ 356
                                     LVCYGFIFRVAR: ...---VKAPFVHCGTVVIVE-EDACFTGPKNS-----STSTSSSG 250
                                                                                                                 VMALVYIMLHSLIGGLEPLFGWSSVEFDEFYMMCVAAWHPEPGYTAFWQIWGALFFFI.VM
                                                                                                                                                                                                                             VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEESSSQM:----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWHKEISYTAFWVTWCCLLPLVAMLVCYGVIFRVARIKARKVY------CGSVVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVEN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAIDRYYAVLYPMIYPMKITGNRAVLAIVYIWLHSLVGCLPPLFGWSSFEFDRFKWTCTV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKFVFSLTSSNLLLSVLMLPFVVASSVRRDWMFGVVWCNFTALLHL--LVSSSSMLTLGA 116
                                                                                                                                                                                                                                                                                                                                            101;
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                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    407 AA; 45363 MW;
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            20.5%; Score 430; DB 4;
29.8%; Pred. No. 1.5e-31;
ative 67; Mismatches 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GEMISHTSTSSSGSPKSLTVSGSQCKAFITTI.VVI.G
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                                                                                                                                                                                                                                                                                                                                                                                                                      00078B8EB5BC1F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407
                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                              135; Indels
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RESULT 5
Q9MZU3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00037; GFCRHODDPSN.

PROSITE; PS00237; G PPOTEIN RECEP P1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Glycoprotein; Transmembrane.

SEQUENCE 425 AA; 47009 MW; 1202C83BF7644CBF CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suzuki F., Taniquchi T., Takauji R., Murata S., Muramatsu I.,
"Splice isoforms of alpha(la)-adrenoceptor in rabbit.";
Br. J. Pharmacol. 129-1569-1576(200)
--- SUBGELLULAP LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL. RF157506; AAF80169.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BREED NEW ZEALAND WHITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha la-adrenoceptor isoform 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9MZU2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9MZU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                 281
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                                                                          340 VLK 142
                                                                                                            358 MLK 360
                                                                                                                                                                                                                                                                                                                                    187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 NSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
                                                                                                                                                                                                                                                                                                                                  GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRO----HALLYNVKRHSLEVRVKDCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIISLCVIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NASDSSNCTH-----PPAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLETWA----TWLSFASAVCHPLIYGLWNKTVRKELLGM 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
                                                                                                                                             FVLCWLPF-FLVMPIGSFFPDFKPPETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN
                                                                                                                                                                               YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
                                                                                                                                                                                                                        KNAPAGGSGVASAKNKTHFSVRL----LKFSREK---
                                                                                                                                                                                                                                                         ENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297
                                                                                                                                                                                                                                                                                                 NEEPGYVLFSALGSFYVPLTIILAMYCPVYVVÄKPESPGLKSGLKTDKSDSEQVTLRIHR 238
                                                                                                                                                                                                                                                                                                                                                                       IDRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISVGPLFGWRQPAPDD-ETICQI-- 178
                                                                                                                                                                                                                                                                                                                                                                                                       VDRYLSIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P02699; 1F88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 15, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.0%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 376; DB 6;
Pred. No. 1.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 425,
                                                                                                                                                                                                                        KAAKTLGIVVGC 280
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                                                                                                                                                                                                                                                                                                                                                         RESULT 6
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Best Local
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01-OCT-2000
01-OCT-2000
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InterFro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; Tut 1; 1.
Pfam; PF00001; Tut 1; 1.
PRONITE; PR00237; GPCREHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; GPROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrand G-protein coupled receptor; GPTB487FCE6DB3B CRC64;
                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BREED NEW ZEALAND WHITE;
MEDLINE=2024335; PubMed=10780960;
Suzuki F., Taniguchi T., Takauji R., Murata S., Muramatsu I.;
"Splice isoforms of alpha(la)-adrenoceptor in rabbit.";
Br. J. Pharmacol. 129:1569-1576(2000).
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Oryctolagus cuniculus (Rabbit) (Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                         Q96RE8
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                  Adrenergic receptor alpha-la.
                                                                                                                                                                                                                                               Q96RE8;
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                                  Homo sapiens (Human)
                                                                    ADRA1A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 FVLCWLPF-FLVMPIGSFFPDFKPPETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 VDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 HYYIVNLAVADLLLTSTVLFFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIISLCVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEEPGYVLFSALGSFYVPLTIILAMYCRVYVVAKPESRGLKSGLKTDKSDSEQVTLRIHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISVGPLFGWRQPAPDD-ETICQI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NASDSSNCTH-----PPAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNAPAGGSGVASAKNKTHFSVPL-
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                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.0%; Score 376; DB 6; 28.1%; Pred. No. 1.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...--LKFSREK
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RESULT 7
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Randriae A G.N., Aarti A.;

"RT-PCP cloning and sequence analysis of adrenergic receptor subtype-
alpha-la cDNA from human prostrate cell-line DU-145.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF395806; AAK77197.1;

EMBL; AF395806; AAK77197.1;

Pfam; PF00001; 7tm 1; 1

Pfam; PF00001; 7tm 1; 1
                               MEDLINE=98149668; PubMed=9490024; Chang D.J., Chang T.K., Yamanishi S.S., Salazar F.H.R., Kosaka A.H., Khare R., Bhakta S., Jasper J.R., Shieh I.-S., Lesnick J.D., Ford A.P.D.W., Daniels D.V., Clarke D.E., Bach C.T., Chan H.W.; "Molecular cloning, genomic characterization and expression of novel human alphalA-adrenoceptor isoforms."; FERS Lett 422:279 283(1998)
                                                                                                                                                                                                                                                                                                01-AUG 1998 (TrEMBLrel 07, Created)
01-AUG-1998 (TrEMBLrel 07, Last sequence update)
01-MAR 2002 (TrEMBLrel 20, Last annotation update)
                                                                                                                                                                                                                   NCBI
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PP0STTF; PS00217; G_PP0TEIN_PECEP_F1_1; UNKNOWN_1.
PP0STTF; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                   Alpha 1A adrenergic receptor isoform 4
                                                                                                                                                                                                                                                                                                                                                          060451;
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NCBI_TaxID=9606;
                                                                                                                                                             TISSUE=PROSTRATE;
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             060451
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SIMILAPITY: RELONGS TO FAMILY 1 OF
                  SUBCELLULAR LOCATION:
                                                                                                                                                                                                                  TaxID-9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAFAGGSGMASAKTKTHESVFL--- LKESREK------KAAKTLGIVVGCF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRO----HALLYNVKRHSLEVRVKDCVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRIQCLCRKQSSKHALGYTLHPPSQAVEG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LK-KFFCKEKPPKE---- DSHPDLPGTEG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEDEEG----AEKKEEFODEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEPGYVLFSALGSFYLFLAIILVMYCFVYVVAKFESFGLKSGLKTEKSDSEQVTLRIHFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRYTGVSHPLPYPTTVTOPPGUMALLCVWALSLVISIGPLFGWPOPA-PEDETTCOI--N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.0%; Score 376;
27.5%; Fred. No. 1
               INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
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G-PROTEIN COUPLED PECEPTORS
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es 171; Indels
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RESULT
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01-NOV-1996 (TREMBLrel 01, Last sequence update)
01-NAR-2002 (TREMBLrel 20, Last annotation update)
Alpha 1C adrenergic receptor isoform 3.
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InterPro; IPP00027; GPCP_Phodpsn
Pfam; PF00001; 7tm 1; 1.
PPINTS; PR00237; GPCRPHODOESN.
PPOSITE; PS00237; GPROTEIN PECEP F1 2; 1.
PROSITE; PS00237; GPROTEIN PECEP F1 2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAPAGGSGMASAKTKTHFSVRL - - - - LKFSREK - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDEEG----AEKKEEFQDEMNIFESLPPSPRNSNSNPPLPFCYQCKAAKVIFIIIFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEPGYVLFSALGSFYLPLAIILVMYCPVYVVAKPESPGLKSGLKTDKSDSEQVTLPIHPK
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26.9%; Fred No. 4.:
tive 77; Mismatche
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Mismatches 180;
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1C-adrenoceptor splice variants.";
FEBS Lett. 363:256-260(1995).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COMPLED RECEPTORS.
EMBL; D32201; BAA06990.1; -.
Interpro; IRR000276; GFCP\_Phodpsn.

PF000001; 7tm

Hirasawa A., Shibata K., Horie K., Takei Y., Obika K., Tanaka T., Muramoto N., Takagaki K., Yano J., Tsujimoto G.;

functional expression and tissue

distribution

of human alpha

MEDLINE=95255557; FubMed=7737411;

TISSUE=PROSTATE,

SEQUENCE OF 424-429 FROM N.A.

Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases

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RESULT 9
Q13675
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Best Local :
                             Diehl N.L., Shreeve S.M.;
"Identification of the alpha 1c-adrenoceptor in rabbit arteries and the human saphenous vein using the polymerase chain reaction.";
Eur. J. Pharmacol. 268:393-388(1994)
                                                                                                                                                                           MEDLINE=95255557; PubMed=7737411;
Hirasawa A., Shibata K., Horte K., Takei Y., Obika K., Tanaka T.,
Muramoto N., Takagaki K., Yano J., Tsujimoto G.;
"Cloning, functional expression and tissue distribution of human alpha
1C-adrenoceptor splice variants.";
Eur. J. Pharmacol. 268:393-398(1994).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                          MEDLINE=95104335; PubMed=7805763;
                                                                                                                              SEQUENCE OF 202-344 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha 1C adrenergic receptor isoform 2. Homo sapiens (Human).
                                                                                                                                                                   FEBS Lett. 363:256-260(1995)
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.

PROSITE; PS50026; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Trisepporter coupled receptor; A77B05C5D60AF69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385
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RA Weinberg D.H., Trivedi P., Tan C.P., Mitra S., Perkins-Barrow A.,
RA Borkowski D., Strader C.D., Bayne M.;
RIT receptors alpha 1a, alpha 1b and alpha 1c.";
RIT receptors alpha 1a, alpha 1b and alpha 1c.";
RI Biochem. Biophys. Res. Commun. 201:1296-1304(1994).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CINTERPOOPEN THEODOPSN.
CR PROVING: PRO00237; GFCRRHODOPSN.
CR PRONTS; PRO00237; GFCRRHODOPSN.
CR PROSITE; PS00237; GFCRRHODOPSN.
CR PROSITE; PS00237; GFCRTEIN RECEPTI 2; 1.
CR PROSITE; PS00237; GFROTEIN RECEPTI 2; 1.
CR PROSITE PRO
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Best Local
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha adrenergic receptor subtype alpha 1C.
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EMBL; S76001; AAD14205.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Ffam; PR00001; 7tm 1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; P800237; G PROTEIN RECEP_F1 1; 1.
PROSITE; P800237; G PROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Glycoprotein; Transm SEQUENCE 499 AA; 55000 MW; BA6E802B6192639D
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94296402; PubMed=8024574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local .
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Pfam; PERONOIS, 7tm 1; 1
Pfam; PERONOIS, 7tm 1; 1
PPINTS; PRO0237; GETPREUNOESE
PRONTTE; PR00237; GETPREUN RECEP_PI_1; 1.
PRONTTE; PS00237; GETPROTEIN RECEP_PI_2; 1.
PROSTTE; PS00262; GETPROTEIN RECEP_PI_2; 1.
PROSTTE; PS00262; GETPROTEIN RECEP_PI_2; 1.
PROTEIN COUNTRY TANNOISE TO STANDARD TO STAN
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"Characterization of the pig alpha-lA adrenergic receptor.";
"Characterization of the pig alpha-lA adrenergic receptor.";
Submitted (PEC-1949) to the EMBL/GenBank/DEBU darabases
1. SUBJECTIVAR LOCATION INTERFAL MEMBRANE PROTEIN (PV SIMILAFITY)
--- SIMILARITY RELONGS TO FAMILY 1 OF G.FROTEIN OCUPLED PROEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metázoa, Chordata, Craniata, Vertebrota,
Mammalia, Euthoria, Cetartipdactyla; Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR 2002 (TrEMBLrel. 20, Last annotation update)
Alpha-1A adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ251727; CAB62570.1; JOINED.
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Local Similarity 26.4%; Pred. No. 7e-25;
hes 107; Concervative 76, Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                    / Match 17.1%; Score 357; DB 6; Length 466; Local Similarity 26.2%; Prod. No. 9.7e-25; Pr
67 NRFIFNLLVTDLLQISLVAFWVVATSVFLFWFLNSHFCTALVSLTHLFAFASVNTIVVVS 126
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                                                                                                            PEPPVMISMAILLGVILGGLIIFGVLGMILVILSVACHRHLHSVT 61
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Best Local :
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Pfam; PF00001; 7tm_1; 1.
PF1NTS; FP00237; GPCPEH-CORDS.
PPINTS; FP00237; GPCPEH-CORDS.
PROSITE; FS60237; GPSCTEIN_PECEF_F1_1; 1
PP0SITE; FS602362; G_PROTEIN_PECEF_F1_2; 1.
G-protein_coupled_receptor; Glycoprotein, Feceptor; Transmembrane
SEQUENCE 408 AA, 45787 MW; 208615677D53B1B5 08064;
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Marracci S., Cini D., Nardi I.;
"Cloning and developmental expression of 5-HTIA receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAP 2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 HT1A receptor
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140 NKRTPRPAAVLISITWIVGFSISIPPMLGWPTP--EDRSDPNACPISEDPGYTIYSTFGA 197
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                                                                                                                                                                                                                                                                                                       81 ISLVAFWVVATSVFLFWFLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYP 140
                                                                                                                                                                                                                                                                                                                                                                                                           24 RCÉVS--YQÍÍASLFÉGESFSÁGIFGNACVIAÁTALEF--SLGNVANYLIGSLAVTDIMV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 KMPISLAHSIIPSTVLVIELAASEVSU - IVLALVISERFESILSVTDEFTERILVTELIS 80
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                                                                                               SEMICERSTILLIGIMIVATECSIPPLYSWSCAAFDERNALISMIWGASFSYTTISVVSF 200
                                                                                                                                                                                              SVLVLPMAAQNQVLNKWTUGQVTCDIF1SLDVLCCTSSIDHUCAIADDRYWAITDPIDYV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVICWLEF ELVMETGSFEEDERBSETVEKIAFWLGYLNSCINETIYECSSQEFFFARQN 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67, Mismatches 168; Indels 59,
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PROSITE; PS00237; GFROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.
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Life Sci. 54:1595-1605(1994)
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01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-UN-2002 (TrEMBLrel 21, Last annotation update)
Alpha 1C-adrencetor, alpha 1C-AR (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94254631; PubMed=8196478; Faure C., Pimoule C., Vallancien G., Langer S.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein coupled receptor; Glycoprotein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of alpha 1-adrenoceptor subtypes present in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UD67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SINGCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 GYSNSLLNPIIYAYFNKDFQSAFKKIIKCKFCRQ 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 FFLOCCIHPYVYGYMHKTIKKEIQDMLKKFFCKE 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 TEAKRKVALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCET-CHMPHLLFDIITWL
                                                                                                                                                                                                                                                  183 LRIHRKNAPAGGSGMASAKTKTHFSVEL-----LKFSPEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 FYIPLILMLVLYGKIFKAAR---FRIRKTVKKAEKKKVADTCLSVSQQSPKEKQRGAQQEL
    353 KEIQDMLKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 IVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNAL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 IVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDEM 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 LLOVINPETENLLVIDLLCISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LHSVTHYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVPCNIWAAVDVLCCTASIMG 65
                                                                                                                                                                                                                                                                                                                     VKDCVENEDEEG----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLFRCYQCKAAKVIF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWL
                                                                                                                                                          IIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIK 352
                                                                                                                                                                                                                                                                                                                                                                                                    CQI--NEEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEVGGAQAQRCVNGATRHGEEGAVLETTEVHHYVNSKCHLHCKPVPPPEQLPPALKNDRA
                                                                                   IVVGCFVLCWLFF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFK
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PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.8%; Score 330.5; DE 27.4%; Pred. No. 2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39361 MW; B4B3C09824EAC734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graham
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                                                                                                                                                                                                                                              KAAKTLG 224
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Best Local
    Q9TTM9;
01-MAY-2000
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01-MAY-1999 (TrEMBLrel 10, Last sequence update)
01-MAR-2002 (TrEMBLrel 20, Last annotation update)
                                                                           6MLL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adrenergic system."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  096716;
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PROSITE; PS00339; AA TRNA LIGASE II 2; UNKNOWN 1.

PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_PECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P29274; 1MMH.
InterPro; IPRO02106; AAtRNA ligaseII
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cardinaud B., Gibert JM., Sugamori K.S., Vincent J.D., Niznik H.B., Vernier P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dopamine D1/beta receptor.

Branchiostoma lanceolatum (Common lancelet) (Amphioxus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Branchiostoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The amphioxus D1/beta receptor and the emergence of the vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   326
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                                                                                                                                                                                                                                                                                                                                                              356 QDMLKKFFCKEK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 FSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 GRL-----EQENNRGKKISLAKEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                     273 GVFILCWLPFFVVNIVNPFCD--RCVQPAVFIALTWLGWINSCFNPIIYAF-----NKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 AIYSDPCLCIFTASTAYTIVSSLISFYIPLLIMLVFYGIIFKAARDQAR-----KINALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 IVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLY-GW-----GQAAF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 LLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNT 121
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                                                                                                                                                                                                                                                                                   RKVFVKMICCHK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRVKDCVENEDEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRTVTNFFIVSLACADLSVGITVLPFAATNDILGYWPFGG-YCDVWVSFDVLNSTASILN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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(TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                   PRELIMINARY;
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25.8%;
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Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 325; DB 5; Length 391; Fred. No. 7.3e-22;
                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 159;
                                                                                   571
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AN Unlen S., Wraith A.;

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"Characterization of the pig alpha-1D adrenergic receptor.";

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"Cloning, functional expression and tissue distription of the alpha IC-adrenergic receptor.";
for the alpha Res. Commun. 195:902-909(1993).
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Gluchowski C.; "Gluchowski C.; "The alpha 1-adrenergic receptor that mediates smooth muscle "The alpha 1-adrenergic receptor that pharmacological properties of the cloned human alpha 1c subtype."; Mol. Pharmacol. 45:703-708(1994).
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Pfam; pF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHJODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
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J. Pharmacol. Exp. Ther. 272:134-142(1995).

-- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
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SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: HEART, BRAIN, LIVER AND PROSTATE,
KILNEY, LUNG, ADRENAL, AORTA AND PITUITARY.
PTM: CARBOXYL-TERMINAL SER OF THP RESIDUES MAY BE PHOS
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7 (POTENTIAL).
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Furness L.M.,
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Branchek T.A.,
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Best Local
                                                                              "Cloning of the rat alpha 1C-adrenergic receptor from cardiac myocytes. Alpha 1C, alpha 1B, and alpha 1D mRNAs are present cardiac myocytes but not in cardiac fibroblasts."; Circ. Res. 75:796-802(1994).
                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
                                                                                                                                                                                                                                                                                                                                                                                                                      A1AA_RAT
P43140;
                                                                                                                                             STRAIN=Sprague-Dawley; TISSUE=Heart muscle;
MEDLINE=95008062; PubMed=7923624;
Stewart A.F., Rokosh D.G., Bailey B.A., Karns L.R., Chang K.C.,
Long C.S., Kariya K., Simpson P.C.;
                                                                                                                                                                                                                                               ADRAIA OR ADRAIC.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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     MEDLINE=95021119; PubMed=7935320; Laz T.M., Forray C., Smith K.E.,
                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   adrenergic receptor).
                                        TISSUE=Brain;
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Forray C., Smith K.E., Bard J.A., Vaysse P.J.,
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S -> T (IN REF. 2).
C -> R (IN REF. 1 AND
T -> P (IN REF. 2).
Q -> E (IN REF. 1).
S -> C (IN REF. 2).
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BY SIMILARITY.
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R PIAM; PRO0237; GPCRRHODDSN.

R PRINTS; PR00237; GPCRRHODDSN.

R PROSITE; PS00237; GPROTEIN RECEP F1 2; 1.

R PROSITE; PS00237; GPROTEIN RECEP F1 2; 1.

R PROSITE; PS00262; G_PROTEIN RECEP F1 2; 1.

R PROSITE PS00262; G_PROTEIN RECEP F1 2; 1.

R PROSITE PS00262; G_PROTEIN RECEP F1 2; 1.

R PROSITE PS00262; G_PROTEIN RECEP F1 2; 1.

R PROSITE PS00262; G_PROTEIN RECEP F1 2; 1.

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"The rat homologue of the bovine alpha 1c-adrenergic receptor shows the pharmacological properties of the classical alpha 1A subtype.";

MO1. Pharmacol. 46:414-422(1994).

-i- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
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                                    187 GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRO----HALLYNVKRHSLEVRVKDCV 242
                                                                                                                      122 IDRYIGVSYPLRYPTIVTORRGVRALLCVWVLSLVISIGPLFGWROPA-PEDETICOI-- 178
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PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%; Score 371; DB 1; 26.1%; Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Mismatches 180;
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PALMITATE (POTENTIAL).
F -> L (IN REF. 1).
N -> G (IN REF. 1).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 466;
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A1AA_M
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                                                                                                                             EMBL;
                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annot or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLISE
G-protein
     PRINTS: PRO0237; GPCRRHODOPSN.
PROSITE: PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE: PS00237; G_PROTEIN_PECEP_F1_2; 1.
PPOSITE: PS50262; G_PROTEIN_PECEP_F1_2; 1.
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of alpha ld-adrenergic receptor and tissue distribution of three alpha l-adrenergic receptor subtypes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CD-1; TISSUE=Brain, and Kidney; MEDLINE-98292316; FubMed=9630362; Xiao L., Scofield M.A., Jeffries W.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C adrenergic receptor).
ADRAIA OR ADRAIC.
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15-JUL-1998 (Rel 36, Created)
15-JUN-2002 (Rel 41, Last sequence update)
15-JUN-2002 (Rel 41, Last annotation update)
                                                                                                                                                 EMBL; AF031431; AAC02658.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chinchetru M A .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alonso Llamazares A., Zamanillo D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96064818; PubMed=7595531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
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"Molecular cloning, expression and characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                 Leurochem 65.2387.2392(1995)

FUNCTION: THIS ALPHA-ADPENEPGIC RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROFEINS THAT ACTIVATE A PHOSPHATIDYLLNOSITOL-ASSOCIATION MESSENGER SYSTEM ITS EFFECT IS MEDIATED BY G(Q)
                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. PTM- CAPBOXYL-TEPMINAL SER OR THP RESIDUES MAY BE PHOSPHORYLATED
                                                                                        ; S80220; AAB47044.1; ALT_INIT
MGI:104773; Adrala.
rPro; IPR000276; GPCP_Phodpsn
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Pharmacol 104:013-221(1948)
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 receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia, Sciurognathi; Muridae; Murinae; Mus
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                           358 MLKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
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VLPIQCLPPPQSSKHALGYTLHPPSQAVEEQHPGMVRIPVGSGETF
                                                                                                                                                                                                                                                                              HYYIVMLAVADLLLTSTVLPESAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMGLCIIS
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                                                      FVLCWLPP-FLVMPIGSFFPNFKPPETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQN
                                                                                YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD
                                                                                                            KNVPAEGSGVSSAKNKTHFSVRL - · · · · LKFSPEK - · ·
                                                                                                                                        ENEDEEG-----AEKKEEFQDEMNIPESLPPSPPNSNSNPPLPPCYQCKAAKVIFIIIFS
                                                                                                                                                                   NEEPGYVLFSALGSFYVPI.TIILVMYCRVYVVAKRESPGLKSGLKTDKSDSEQVTLRIHR
                                                                                                                                                                                            GASPSYTILSVVSFIVIFLIVMIACYSVVFCAARRO....HALLYNVKRHSLEVPVKDCV
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               51762 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     17.6%;
27.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                Score 368; DD _. NO. 1.6e-16;
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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5 (POTENTIAL)
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2 (FOTENTIAL)
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PALMITATE (POTENTIAL)
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7 (POTENTIAL).
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3 (POTENTIAL).
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A1AA
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SEQUENCE FROM N.A.
                               Cavia porcellus (Guinea pig).
Eukaryota; Metazoa, Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
                                                                                                                                                                  CAVPO
                                                                                                                             Q9WUZ5;
16-OCT-2001
                     NCBI_TaxID=10141;
                                                                    ADRA1A
                                                                                adrenergic receptor).
                                                                                                                                                        Alaa CAVPO
                                                                                                                               (Rel. 40,
                                                                                                                                                        STANDARD;
                                                                                                                                 Created)
                                  Craniata, Vertebrata, Euteleostomi,
Hystricognathi; Caviidae; Cavia.
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CARBOHYD
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR000237; GECRRHODDPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1 1; 1.

PPOSITE; PS00237; G_PROTEIN_RECEP_F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and functional expression of the alpha (la) -adrenoceptor ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gonzalez-Espinosa C., Romero-Avila M.T., Mora-Rodriguez D.M., Gonzalez-Espinosa D., García-Sainz J.A.;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                  247
                                                                                                                                123
224 ---TDKSDSEQVTLFTHFKNAPLGGSGVASSKNKTHFSVRLLKFSPEKKAAKTLGIVVGC 280
                                                                 180
                                                                                                188
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J. Phatmacol. 426:147-155(2001).

FUNCTION: THIS ALPHA-ADRENERGIC PECEPTOR MEDIATES ITS ACTION BY ASSOCIATION MITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q) AND G(11) PROTEINS (BY SIMILARITY).

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILAPITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                           DRYIGVSYPLRYPTIVTQRRGLRALLCLWALSLVISIGPLFGWRQPA-PQDETICQI--N
                              EFGAEKKEEFQDEMNIPESLPP-----SPPNSN--SNPPLPRCYQCKAAKVIFIITES 297
                                                                                            ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ-HALLYNVKRHSLEVRVKDCVENED 246
                                                                                                                                                            DRYLSIIHPLSYPSKMTQPRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
                                                                                                                                                                                             YYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMSLCIISI 122
                                                                                                                                                                                                                           RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
                                                                                                                                                                                                                                                            SGNASDSSNCTQP--PAPVNIPKAILLGVILGVLILFGVPGNILVILSVACHRHLHSVTH 62
                                                                                                                                                                                                                                                                                           STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
                                                               EDPSYVLFSALGSFYVPLAIILVMYCRVYVVAKRESRGLTSGLK-----
                                                                                                                                                                                                                                                                                                                               106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF108016; AAD22540.2;
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                               466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              330
                                                                                                                                                                                                                                                                                                                               Conservative
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54
90
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                                                                                                                                                                                                                                                                                                                                         17.5%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                             51577 MW;
                                                                                                                                                                                                                                                                                                                             75; Mismatches
                                                                                                                                                                                                                                                                                                                                           Score 366.5; DE Pred. No. 2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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2 (POTENTIAL
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-LINKED (GLCNAC. . .) (P
E0E27E4FF5D3D0CD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palmitate
                                                                                                                                                                                                                                                                                                                                                           Length 466;
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                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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           TRANSMEM
DOMAIN
                                                      DOMAIN
TRANSMEM
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                                                                                                                   PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
                                                                                                          Multigene
                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia, Eutheria, Cetartiodactyla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 TRANSMEM
                                        DOMAIN
                                                                                TRANSMEM
                                                                                            DOMAIN
                                                                                                                                                               PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                          InterFro; IFR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                        PIR; A35375; A35375.
                                                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92087349; PubMed=1966743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADRA1A OR ADRA1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adrenergic receptor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                                                                                 AND G(11) PROTEINS.

SINCELLULAR LOCATION: Integral membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YVLSLGFYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
                                                                                                                                                                                                                     J05426; AAA30374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chem. 265:8183-8189(1990).
                                                                                                         family;
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                                                                                            Phosphorylation; Lipoprotein; Palmita 27 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                   CYTOPLASMIC
2 (POTENTIAL
                                                                                1 (POTENTIAL)
                                                      (POTENTIAL)
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Best Local :
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                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Pel. 35, Last sequence update)
01-NOV-1997 (Pel. 35, Last annotation update)
Alpha-la adrenergic receptor (MARI).
07y2138 latipes (Medaka fish) (Japanese ricefish)
07y2138 latipes (Medaka fish) (Japanese ricefish)
07y2138 latipes (Medaka fish) (Japanese ricefish)
07y2138 latipes (Medaka fish) (Japanese ricefish)
07y2138 latipes (Medaka fish) (Fercomorpha, Euteleostei, Mecteleostei,
07y2138 Accanthomorpha, Acanthopterygli; Fercomorpha, Atherinomorpha,
07y2138.
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MEDLINE-96184522; PubMed-8654394; Yasuoka A., Abe K., Arai S., Emori Y.; Yasuoka A., Abe K., Arai S., Emori Y.; "Melecular cloning and functional expression of the alphala adrenoceptor of Medaka fish, Oryzias latipes."; Eur. J. Biochem. 235:501-507(1996)
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Q91175;
G1-NGV-1997 (Fel
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                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                            NCBI_TaxID=8090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENEDEEG....AEKKEEFQDEMNIFESLFFSFFNSNSNFPLFFCYQCKAAKVIFIIIFS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEEDGYVLFSALGSFYVPLTTILVMYCPVYVVAKPESPGLKSGLKTDFSDSEQVTLFIHF
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25.5%; Pred No. 8;
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Query Match
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PHAM: PRONOL; 7tm 1; 1.

PRINTS, PRO0237; GECRHODOPSN.

PROSITE; PS00237; GEPOTEIN PROCEP F1 1; 1

PROSITE; PS00237; GEPOTEIN PROCEP F1 2; 1

Geprotein coupled receptor; Transmombrane; Glycoprotein,

Geprotein coupled receptor; Transmombrane; Glycoprotein,

Multigene family, Phospherylation; Lipoprotein; Palmitate.

Multigene family, Phospherylation; Lipoprotein; Palmitate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D63859; BAA09921.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: THIS ALFHA-ADRENESGIC FECEFTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
                                                                                                                    LRMH RGNTTVSEDEALRSRTHFALRLLKFSREKKAAKTLGIVVGCFVLCWLP--FFLVL
                                                                                                                                                                                                                                                                                                                                                             GVSYPLPYPAIMTKPPALLAVMLLWVLSVIISIGPLFGWKEPA-PEDETVCKIT--EEPG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEAVADELESSTVEFSAIPEILDEWVFGEVFCNIWAAVDVECCTASIMSECVISVDFYI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNCSHVLAP----ELNTVKAVVLGMVLGIFILFGVIGNILVILSVVCHRHLQTVTYYFIV 66
                                                                                                                                                                             KKEEFQDEMNIFESUPPSPRINNSNPPUPPCYQCKAAKVIFIIIFSYVUSUSPYOFLAVU RII
                                                                                                                                                                                                                                            YAIFSAVSSFYLFLAIILAMYCEVYVVAQKE····
                                                                                                                                                                                                                                                                                                                                                                                                                   SITHPLSYPSKMTQERGYLLLYGTWIVAILQSTPPLYGWGQAAFDEPNALGSMIWGASPS 191
PIGSIFFAYRESETVEKİTEWLGYFKSCİMETIYLCSKQEFYKAFÇOLL-GVHCLBMIFR
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470 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.9%; Score 354; DB 1; 28.0%; Pred. No. 1.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Mismatches 193; Indels
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N-LINEED (SLOWAC. ) (POTENTIAL)
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"Molecular cloning of 5-hydroxytryptamine (5-HT) type 1 receptor genes from the Japanese puffer fish, Fugu rubripes.";

Gene 191:219-223(1997).

-i- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYFEMAINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Integral membrane protein.

-i- SUBCELLULAR LOCATION: TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                     CARBOHYD
                                                      CARBOHYD
                                                                     DISULFID
                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                       Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fugu rubripes (Japanėse pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
5-hydroxytryptamine 1A-alpha receptor (5-HT-1A-alpha) (Serotonin receptor) (5-HT1A-alpha) (FIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDI.INE=97361762; PubMed=9218723;
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30-MAY-2000 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    PF00001; 7tm
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107
   47000 MW;
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                N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                BY SIMILARITY.
                                                                               CYTOPLASMIC
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                                                                                                                  Life Sci. 47:127-132(1990).

-!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
-!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
-!- FUNCTIONS
AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90202832; PubMed=2156831;
Albert P.R., Zhou Q.-Y., van Tol H.H.M., Bunzow J.R., Civelli "Cloning, functional expression, and mRNA tissue distribution rat 5-hydroxytryptaminelA receptor gene.",
J. Biol. Chem. 265:5825-5832(1990).
                                                                                                                                                                                                                           erythropoietin.";
                                                                                                                                                                                                                                 "Role of cytochrome P450 in the control of the production of
                                                                                                                                                                                                                                                                            Fujiwara Y., Nelson D.L., Kashihara K., Varga B.,
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90355775; PubMed=2167416;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
5-hydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor)
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01-NOV-1990
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                                        SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.
                                                                                                            CYCLASE ACTIVITY
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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PP1NTS; PF00001; /rm 1; 1
PROSITE; PF000237; G_PEOTEIN_RECEP_F1 1; 1:
PROSITE; PS000237; G_PEOTEIN_RECEP_F1 2; 1:
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Military Coupled receptor; Transmembrane;
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PIR; JH0315; JH0315.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The alpha 1-adrenergic receptor that mediates smooth muscle contraction in human prostate has the pharmacological properties the cloned human alpha 1c subtype."; mol Pharmacol. 45:703-708(1994).
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MEDLINE=94239386; PubMed=8183249;
Porray C., Bard J.A., Wetzel J.M., Chit
Lepor H., Hartig P.R., Weinshank R.L.,
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16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-1D adrenergic receptor (Alpha-1P-adrenoceptor) (Alpha-1A
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MEDLINE-95365059; PubMed=7746384;
Esbenshade T.A., Hirasawa A., Tsujimoto G., Tanaka T.,
Minneman K.P., Murphy T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adrenergic recept other species homologues.";
other species homologues.";
other 572 134-142(1995).
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Schwinn P A , Johnston G I , Page
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MEDLINE=92028892; PubMed=1656955;
Bruno J.F , Whittaker J., Song J., Berelowitz M.;
"Molecular cloning and sequencing of a cDNA encoding
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Piochem Biophys. Pes
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ADPA1D OR ADRA1A
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                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                         Mol. Pharmacol. 47:977-985(1995).
I FUNCTION: THIS ALPHA-ADPENERGIC PECEPTOR MEDIATES
THROUGH THE INFLUX OF EXTRACELIBRAR CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of the human alpha 1d-adrenergic receptor and inducible expression of three human subtypes in SK-N-MC cells.";
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                          SWISS PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics, and the EMBL outstation
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Branchek T.A.,
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EMBL; L31772; AAB59487.1;

EMBL; S70782; AAB31163.2;

EMBL; D29952; BAAC6222.1;

EMBL; D29952; BAAC622.1;

EMBL; D40447; JH0447;

Genew; HGNC:280; ADRAID.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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KPPSAFREWRLLGPFRRPTTGLRAKVSSLSHKIRAGGAQR
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KEPSACAQRSEVEAVSLGVPHEVAEGATCQAYELADYSNLR
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MTFRDLLSVSFEGPRPDSSAGGSSAGGGGGSAGGAAPSEG
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PROSITE; FS00237; GFROTEIN_RECEP_F1_1, 1.
PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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Pfam; PF00001; 7tm_1; 1.
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                                     Length 416;
                                                                                    CRC64;
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Conservative

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Mismatches

Indels

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IS-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Pel. 36, Last sequence update)
15-JUN 2002 (Rel. 41, Last annotation update)
Alpha-10 adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                       WEDLINE-94116980, PubMed-8288218,
Wilkie T.M., Chen Y., Gilbert D.C., Moore E.J.,
Chenhard N.G., Jenkins N.A.,
"Identification, phromosomal location, and genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of alpha id-adrenergic receptor and tissue distribution of three alpha 1-adrenergic receptor subtypes in
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mammalian G-protein-coupled receptors.";
Genomics 18:175-184(1993).
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Chinchetru M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria, Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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Eutheria, Rodentia; Sciurognathi; Muridae, Murinae; Mus
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PPOSITE; PS00262; GPPOTEIN PECEP_F1 2; 1

PPOSITE; PS00262; GPPOTEIN PECEP_F1 2; 1

G-protein coupled receptor; Transmembrane, Glycoprotein;

G-protein coupled receptor; Transmembrane, Glycoprotein;

G-protein coupled receptor; Transmembrane, GPOTENTIAL).

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                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
COMAIN
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! SUBCEPLULULAR LOCANION: Integral membrane protein
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COURLED PECEPTORS
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EMBL, AB030641; BAA90312.1; JOINED
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Pfam; PF00001; 7tm_1; 1
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312 NPGTQSSKGHTLESSLSVPLLKFSREKKAAKTLAIVVGVEVLCWEPEFFVLPLGS-LFPQ 370
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                                                             IVVMYCRVYVVARS
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                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                          PALMITATE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                 6CF15S15B5F7FA47 CFC64;
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                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                      164; Indels
                                                                                                                                                                                                                                                                                                                                 Length 562;
                                                                                                                                                                                                                                                                                                      :10
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                       263
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319

TQVPQWVITIIIWLFFLQCCTHPYVYGYMHKTIKKEIQDMLK 360

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                                                                                                                                                                                                     EMBL; M28269; AAA36440.1; ...
EMBL; X13556; CAA31908.1; ...
EMBL; X57829; CAA40962.1; ...
EMBL; M83181; AAA66493.1; ...
PIR; S07343; S07343; S07343; S07343; S07343; S07343; S1438; S31438; 3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S3148; S31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawanishi Y., Harada S., Tachikawa H., Okubo T., Shiraishi H.;
"Novel mutations in the promoter and coding region of the human 5-HTIA receptor gene and association analysis in schizophrenia.";
Am. J. Med. Genet. 81:434-439(1934)
--!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYFTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMME outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
InterPro; IPR000276; GPC
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                     MIM;
                                                                                                                                                          Genew; HGNC:5286; HTR1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P08908; Rel. 09, Created)
01-NOV-1988 (Rel. 09, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5-hydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor) (5-HT1A) (G-21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genomic clone G-21 which resembles a beta-adrenergic receptor sequence encodes the 5-HTIA receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98425601; PubMed=9754630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88334700; PubMed=3138543;
Fargin A., Raymond J.R., Lohse M.L., Kobilka B.K., Caron M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT ASP-272.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87315369; PubMed=3041227; Kobilka B.K., Frielle T., Collins S., Yang-Feng T.L., Kobilka T.S., Francke U., Lefkowitz R.J., Caron M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saltzman A.G., Morse B., Felder S.;
Submitted (FEB-1991) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRONGEST TO THE OTHER SHT-1 SUBTYPE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                          109760;
                                     IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
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Best Local :
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331 WLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKE 366
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                        267 VESKAGGALCANGAVRQGDDGAÁLEVIEVHRVGNSKEHLFLFSEAGFTFCAPASFERKNE 326
                                                                                                                                     207
                                                                                                                                                                          149 TPRRAAALISLTWIIGFLISIPPMLGWRTP--EDRSDPDACTISKDHGYTIYSTFGAFYI 206
                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                  204 PLIVMIACYSVVFCAAR-RQHALLYNVKRHSLEVR---
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DOMAIN
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Polymorphism.

DOMAIN

1 36 EXTRACEPTATION (POTENTIAL)
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                                                                                                                                                                                                                                                  84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
                                                                                                                                                                                                                                                                          31 VTVSYQVİTSLILİGTLIFCAVLÖNACVVAAIALER--SLQNVANYLIGSLAVTDLMVSVL 88
                                                                                                                                                                                                                                                                                                   26 ISLAHGIIRSTVLVIFLAASEVGN--IVLALVLQRKEQLLQVTNREIENLLVTDLLQISL 83
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                       RNAEAKRKMALARERKTVKTLGİİMGTFILCWLÞFFIVÁLVLÞECESSCHMPTLLGAİİN 386
                                              RNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIII 330
                                                                                               PLLLMLVLYGRIFRAARFRIRKTVKKVEKTGADTRHGASPAPQPKKSVNGESGSRNWRLG 266
                                                                                                                                                                                                 TQRRGYLLLYGTWIVAILQSTEPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI 203
                                                                                                                                                                                                                         VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148
                                                                                                                                                                                                                                                                                                                                      95;
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                                                                                                                                                                                                                                                                                                                                                                                    422 AA;
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378
403
                                                                                                                                                                                                                                                                                                                                                                                      46106 MW;
                                                                                                                                                                                                                                                                                                                             15.4%; Score 321.5; DB 1; Length 24.0%; Pred. No. 1.2e-13; tive 72; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                              M -> I (IN REF. 1).
K -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR_011830.
RAA -> PR (IN REF. 1).
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G -> D (IN DBSNP:1800042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P -> L (IN DBSNP:1800043)
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I -> V (IN DBSNP:1799921).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR_011829.
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R -> L (IN DBSNP:1800044)
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G_-> S (IN_DBSNP:1799920)
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P -> L.
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7 (POTENTIAL)
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(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
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"Identification, chromosomal location, and genome organization of mammalian G-proteoin-coupled recoptors.";

Genomics 18:175-184(1993)
Genomics 18:175-184(1993)
Genomics 18:175-184(1993)
A DIFFERENT EECEPTORS FOR 5:
HYDEOXYTPYFAMINE (SEFOTENIN), A BIOGENIC HORMONE THAT FUNCTIONS AS A NECECTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5-bydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bicinformatics and the EMBL cutstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no use by non-profit institutions as long as its content is in no use by non-profit institutions as long as its content is in no use by non-profit institutions as long as its content is in no use by non-profit institutions as long as its content is in the long that the long that it is not removed. Usage by and for roomer than the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the long that the l
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                                                                                                                                      InterPro; IPP000276; GPCP_Phodpsn
Pfam; PF00001; 7tm_1; 2
PPINTS; PP00237; GPCPPHODOPSN
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MEDLINE 94116980; FubMed-9298218.
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Mammalia, Eurheria, Endentia, Schurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                  MGD; MGI:96273; Htrla.
                                                                                                                                                                                                                                                                                                                 EMBL; U33820; AAC52572.1;
EMBL; L20339; AAA16850.1;
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; [139391; AAA81519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J Riol Them 271:4417-4430(1996).
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J. Neurosci. 13.5164 5171(1993).
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MEDLINE=94076019, PubMed=8254366;
   Multigene family.
                             pposite; pson2x7; G_ppotein_pecep_ei_; i.
procite; pssonen; G_ppotein_pecep_ei_; i.
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01-NOV1990 (Rel. 16, Created)
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15-JUL-1998 (Pel. 36, Last annotation update)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                              Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor)
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                                                                                                                                               STANDARD;
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24.3%; Pred. No. 1.
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Sciurognathi; Muridae;
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                Craniata; Vertebrata; Euteleostomi;
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Mesocricetus

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Matches
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PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN RECEP F1_1; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1_2; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1_2; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1_2; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1_2; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Constitutive activation of the alpha 1B-adrenergic receptor by all amino acid substitutions at a single site. Evidence for a region which constrains receptor activation.";
J. Biol. Chem. 26:7:1430-1433 (1992).
-!- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
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Pfam; PF00001; 7tm_1; 1.
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14 SSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNL 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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MEDLINE=92112850; PubMed=1346134;
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Caron M.G., Kobilka B.K.;
"Molecular cloning and expression of the cDNA for the hamster alpha
D-adrenergic receptor.";
                                                                              Local
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                                                               92;
                                                                  15.2%; Score 319; DB 1; Similarity 26.0%; Pred, No. 2.1e-13;
                                                           Conservative
                                                                                                                            515 AA;
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71
84
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183
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                                                        70; Mismatches
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EXTRACELLULAR (POTENTIAL)
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Search completed: February 11, 2003, 11:08:31 Job time : 16 secs

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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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AAM51646
                                                                                                                                                                                       Human; G protein-coupled receptor; nGPCR-2644; infection; gene therapy; human immunodeficiency virus; HIV; cancer; diabetes; inflammation; cardiovascular disorder; neurological disorder; rheumatoid arthritis; autoimmune disorder; hormonal disorder; renal failure; psoriasis; asthma.
                                                                                                                                  01-NOV-2001.
                                                                                      25-APR-2000; 2000US-199558P.
                                                                                                           25-APR-2001; 2001WO-US13249.
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                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                  Human nGPCR-2644 polypeptide.
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Novel G protein-coupled receptor-2644 nucleic acid molecule and

WPI; 2002-041396/05. N-PSDB; ABA03782.

Lind P,

Sejlitz T,

(PHAA ) PHARMACIA & UPJOHN CO.

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Best Local:
               Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia; attention deficit disorder; anxiety; depression; bipolar disorder; neurological disorder; huntington's disease; dementia; obesity; ancrexia metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer; cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV; viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;
antidepressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a gene encoding a novel G protein-coupled receptor designated mGPCR-2644 mGPCR-2644 polynuclectide and polypeptides, and antibodies against mGPCR-2644, are useful for reating diseases such as viral infections caused by human immunodeficiency virus (HIV)-1 or HIV-2, pain, cancers, diabetes, chesity, ancrexia, hypotension, hypertension, thrombosis, myocardial infarction, cardiomyopathies, atheroselerosis, parkinson's disease, schizophrenia, migraine, anxiety, manic depression, dementia, Huntington's disease, thyroid disorders, inflammatory conditions, the manic depression of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of the condense of t
                                                                                                                                                                                           Human G Protein-Coupled Receptor (GPCR) polypeptide #52.
                                                                                                                                                                                                                                                                                                                          AAU25605 standard; Protein; 508 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 31; Page 60; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides encoded by them, useful for treating cancers, psoriasis, Alzheimer's disease, atherosclerosis, rheumatoid arthritis, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         renal failure, psoriasis, movement disorders, asthma and traumat:
brain injury. The present sequence is the nGPCR-2644 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis, autoimmune disorders, hormonal disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLGPYCFLAVLAVWYDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVENEDEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVENEDEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                    KFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
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  anorectic;
gene therapy
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                                                                                   thrombosis;
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23-FEB-2000; 2000US-0184303.
23-FEB-2000; 2000US-0184305.
23-FEB-2000; 2000US-0184395.
23-FEB-2000; 2000US-0184397.
02-MAR-2000; 2000US-0186810.
09-MAR-2000; 2000US-0186810.
09-MAR-2000; 2000US-0186806.
13-MAR-2000; 2000US-018880.
03-APR-2000; 2000US-018880.
03-APR-2000; 2000US-018861.
11-UUL-2000; 2000US-0213861.
11-UUL-2000; 2000US-0213370.
14-UUL-2000; 2000US-0219337.
20-JUL-2000; 2000US-02193492.
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                    181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD 240
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                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               508 AA;
                                                                                                                                                                                                                                                                                                                            Conservative
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78.1%;
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(GFCR) polypeptides of the invention. The proteins and their associated DNA sequences can be used to identify compounds which bind to GFCR polypeptides and in screening for compounds that modulate GFCR activity. By screening a human subject for the presence of mutations in GFCR DNA, GFCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, dementia and bipolar disorder, neurological disorders such as huntington's disease, Parkinson's disease and Tourette's syndrome, metabolic disorders such as obesity, anorexia and type 2 diabetes, cardiovascular disorders such as thrombosis, myocardial infarction, cardiovyopathy and atherosclerosis, viral infections caused by HIV and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAU25554-AAU25616 represent human G-protein coupled receptor (GPCR) polypeptides of the invention. The proteins and their associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders, such as schizophrenia, anxiety, depression, or obesity
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                                                                                                                                                                            QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
                                                                                                                                                                                                                                                                                                                     MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
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TIVVVSVDPYLSIIHPLSYPSKMTQPPGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
                                                                                                        QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2024; DB 22;
Pred. No. 3.8e-204;
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RESULT 3
AAB86428
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Best Local
                                                                                                                                                             This invention describes a novel human brain-derived G protein receptor gene and its encoding protein, designated SERALPHA. The receptor or cells expressing the receptor are used to develop new medicines, chemicals and technologies, and to devaluate existing medicines and technologies.
                                                                                                                                                                                                                                              Disclosure; Page 4; 8pp; German.
                                                                                                                                                                                                                                                                                     Gene encoding a protein of the G protein receptor super family, having homology to neurotransmitter receptors is useful to develop new medicaments -
                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                  Bruess M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000DE-1004930
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                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                   medicaments
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   MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
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                                                                   397;
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                                                                                                                                 508 AA;
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                                                                               96.7%;
78.1%;
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                                                              Score 2024; DB 22;
Pred. No. 3.8e-204;
1; Mismatches 0;
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28-APR-2000
11:-WAY-2000
11:-UNN-2000
11:-UNN-2000
21-AUG-2000
26-SEF-2000
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23-DEC-1999;
23-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; G-protein coupled receptor; GPCR; hRUP15; agonist;
inverse agonist; lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human G-protein coupled receptor, hRUP15.
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14-MAR-2000;
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17-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents a human G-protein coupled receptor (GPCR)
                  EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
                                                                     L'AVMADAELÖADÖMALLI I MTELTÖCCIH BAAAAANI KKEI ÖDWIKKEECKEK BEK
                                                                                  LAVWYDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
                                                                                                                                          MESEDDVEAVNIPESTEPSPENSNSNPPLPRCYQCKAAKVIFITIFSYVLSLGPYCFLAV
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EDSHPDLPGTEGGTEGKIVPSYDSATFP 508
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78.1%;
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Pred. No. 3.8e-204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to nine human guanosine triphosphate binding protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16, GPRv21, GPRv40, GPRv47, GPRv47, GPRv51, GPPv71 and GPPv72, and to the genes encoding them. These genes and proteins and antibodies against the protein are useful in the treatment, prevention, diagnosis and investigation of diseases associated with G protein-coupled receptors, including cancer, cirrhosis of the liver and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA encoding guanosine triphosphate binding protein coupled receptors and their expression products for screening potential anticancer and nootropic drugs and in diagnosis of these diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; guanosine triphosphate binding protein-coupled receptor; gprotein-coupled receptor, GFFv8; GFFv12; GFFv16; GFFv21; GFRv70; GFFv47; GFFv51; GFFv71; GFFv72; cancer, liver cirrhosis, Alzheimer's disease; cytostatic; hepatotropic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 135-138; 170pp; Japanese
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                                 CVENEDEEGAEKKEEFQDE -----
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78.1%;
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o T, Kanzaki K, Yasuda S, Inoue
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Pred. No. 3.8e-204;
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                    The invention relates to an isolated polynucleotide encoding an alphala adrenergic receptor-like G-protein coupled receptor (GPCR) polypeptide, the encoded polypeptide, fragments, derivatives and allelic variants. Also include are an expression vector comprising the polynucleotide, a host cell containing the vector, screening for therapeutic agents which decrease or increase the activity of the receptor by binding a test agent to the protein and determining whether the activity is deceased or increased. A modulator of the receptor is useful for treating alphala adrenergic receptor-like GPCR disorder such as peripheral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPCR; peripheral nervous system disease; central nervous system disease; urinary incontinence; benign prostatic hypertrophy; infection; HIV infection; human immunodeficiency virus; pain; cancer; anorexia; bulimia; asthma; Parkinson's disease; obesity; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; psychosis; neurological disorder; anxiety; schizophrenia; manic depression; delirium; dementia; severe mental retardation; dyskinesia;
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04-DEC-2000; 2000US 250505P.
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Fig 3; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha (la) adrenergic receptor-like G-protein coupled receptor (GPCR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide, useful for treating pain, cancer, Parkinson's diseases, obesity, hypertension, asthma, schizophrenia, encodes as
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central nervous system disease, urinary incontinence or benign prostatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to disease and abnormalities related to the presence of mutations in the gene. The protein is useful to identify test compounds which may act as agonists or antagonists, and for raising antibodies which can block the receptor and effectively prevent ligand binding. The present sequence is the alphala adrenergic receptor-like GPCR.
                                       G-protein coupled receptor; GPCR; hRUP15-Gs; agonist;
                                                                                 GPCR-Gs fusion protein, hRUP15-GS
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                                                                                                                              23-OCT-2001 (first entry)
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                  inverse agonist; lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer Non-endogenous version of human GPCRs are also utilized in resear
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TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
                           TIVVVSVIPYLSIIHPLSYPSYMTQRPGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
                                                                                                      QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
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This represents a G-protein coupled receptor family polypeptide, IGS1. The IGS1 protein can be expressed by standard recombinant methodology. IGS1 is useful for inducing immunological response in a mammal, as vaccine. IGS1 polynucleotides and polypeptides and its modulators are useful for treating psychiatric and central nervous system disorders especially movement disorders, such as tics, tremor, Tourette's syndrogeneral percentages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              movement disorder; tremor; Tourette's syndrome; Parkinson's disease; Huntington's disease; dyskinesia; dystonia; spasm; neuroleptic; huma nootropic; anticonvulsant; relaxant; vaccine; gene therapy.
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                                                                                                                                                                             Novel human G-protein coupled receptor family polypeptide, IGS1, useful for treating psychiatric and central nervous system disorders such as tics, tremor, Tourette's syndrome and Parkinson's disease -
                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-2000; 2000WO-EP06878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human G-protein coupled receptor,
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99NL-1012611.
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gene therapy.
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Parkinson's disease, Huntington's disease, dyskinesias,

Tourette's syndrome. dystonia

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                                                                                                                                                                                                                   G-protein coupled receptor; receptor; AXOR69; human; anti-HIV; virucide; antimicrobial, analgesic; cytostatic; antidiabetic; anabolic; antissthmatic; antiparkinsonian; cardiant; cerebroprotective; hypotensive; hypertensive; antidicer; antiasteria; antiemetic; tranquillizer; neuroleptic; antiasthmatic; antiallergic; antiemetic; tranquillizer; neuroleptic;
                                                                                                                                                                                                                                                                                                                      G-protein coupled receptor AXOR69.
                                                                                                              03-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                     ABB75712 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
(SMIK) SMITHKLINE BEECHAM CORP (SMIK) SMITHKLINE BEECHAM PLC.
                                                                            12-JUN-2001; 2001GB-0014287
                                                                                                                                                                                                          nootropic; anticonvulsant; vaccine.
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                                            16-JUN-2000; 2000US-0596400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDSHPDLPGTEGGTEGKIVPSYDSATFP 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 480
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78.0%;
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Pred. No. 7.8e-204;
Pred. No. 7.8e-204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family, such as human adrenergic alpha-la receptor. The invention provides AXOR69 polypeptides and polypucticetides, and methods for producing such polypeptides by recombinant techniques. Also provided are methods for using the AXOR69 polypeptides and polypucticetides to screen for compounds that stimulate or inhibit AXOR69 levels or activity. The polypeptides, polypuctotides, agonists and antagonists are used to treat conditions associated with AXOR69 imbalance, including bacterial, fungal, protozoan and viral infections, particularly HIV-1 and HIV-2 infections, pain, cancer, diabetes, obesity, ancrexia, bulimia, asthma, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation, and dyskinesias such as Huntington's disease and Gilles de la Tourette syndrome. AXOR69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides are also useful in vaccines, and for raising specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An isolated human G-protein coupled (7TM) receptor AXOR 69 polypeptide, for treating diseases such as obesity, stroke and anxiety -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL53719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 27; 34pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                              181
371 EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
                                                                                 311 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
                                                                                                                                   361 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV
                                                                                                                                                                                                                       301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360
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                                                                                                                                                               ------MNI PESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGBYCFLAV
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                                            LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   that shows homology to other members of the GPCR human adrenergic alpha-la receptor. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shabon U;
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Pred. No. 7.8e-204;
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DB 22;

Length 508;

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12-MAY-2000;
12 JUN-2000;
12 JUN-2000;
21 AUG-2000;
26-SFP-2000;
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17-NOV-1999;
17-NOV-1999;
                                    versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agenists or partial agenists having applicability as therafeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors
 Sequence
                                                                                                                                                                                                          Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-APR-2000;
10-APR-2000;
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inverse agonist; lung cancer; A398K; mutant; mutein
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                         play in the human condition, both normal and diseased
                                                                                                                                                                    Claim 30, Page 141, 160pp, English.
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19 AFE-2000;
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                                                                                                                                                                                                                                                PSDB; AASO8265
                                                                                                                             sequence is a human G-protein coupled receptor (GPCP), hRUP15, BK. The endogenous and non-endogenous, constitutively activated
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                                                                                                                                                                                                                                                             2001-355616/37.
                                                                                                                                                                                             agonists or partial agonists for use as therapeutic agents
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  508 AA;
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2000US-0189259,
2000US-0195898,
2000US-0195899,
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Best Local .
                                                                                                                                                                                                                                                            Human; seven transmembrane domain receptor; 65499; 58875; cytostatic; receptoripathic; vasciropic; cardiant; antipsoriatic; antithyroid; receptor; neuroprotective; antipathinsonian; antidiabetic; virucide, analgesic; actificematic, antiarthritic, anorectic, immunomodulator; gene thorapy
                                                                                                                                                                                                                                                                                                                               Human seven transmembrane receptor, 65499 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   ABP079Rs standard; Protein;
             N-PSDB; ABL41163, ABL41164.
                            WPI; 2002-444096/47
                                                         Gluckmann
                                                                                                                                           03-00T-2001; 2001WO-US31250
                                                                                                                                                                         11-APR-2002
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                                                                                   (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLLQVTNRFIENLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAVWVDVETQVPQWVITIIIWLFFLQCCIHFYVVGYMHKTIKKEIQDMLKKFFCKEKPPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396;
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78.0%,
                                                                                                                                                                                                                                                                                                                                                                                                                        508
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Fred. No. 1.3e-203;
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Matches 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease,), brain disorders (e.g., multiple sclerosis, Parkinson's disease,), hormonal disorders (diabetes mellitus, hyperthyroidism,), immune disorders (including autoimmune diseases such as rheumatoid arthritis, osteoarthritis,), liver disorders, viral diseases such as hepatocellular cancer, pain disorders (e.g., pain associated with surgery or chest pain,), metabolic disorders (obesity, cachexia,). The 65499 or 58875 molecules are useful as surrogate markers, as pharmacodyanamic markers and as pharmacogenomic markers. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders (including cancer e.g., carcinoma, sarcoma), bone metabolism disorders (e.g., osteoporosis, rickets,), haematopoletic disorders (such as chronic myelogenous leukemia, acute promyeloid leukemia,), cardiovascular disorders (e.g., ischaemic heart disease, myocardial infarction, etc), endothelial cell disorder (e.g., psoriagis, Grave's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel seven transmembrane domain receptors, designated 65499 or 58875. The 65499 and 58875 polypeptides can be expressed by standard recombinant methodology. The polypeptides, encoding polynucleotides and modulators are useful for controlling G protein coupled receptor-related disorders, and as a novel diagnostic target and therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated 65499 or 58875 polypeptide, novel seven transmembrane domain receptors, useful as reagents or targets for treatment or diagnosis of rheumatoid arthritis, ischemic heart disease, Grave's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 1a-b; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease, obesity
481
                                                                        371
                                                                                                                                                421
                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                260
                                                                                                                                                                                                                                                                                                                                                                                                                                    301
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RGSEEVPESSTVASDGSMEGFEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVENEDEEGAEKKEEFQDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAAPPQHALLYNVKPHSLEVP.VKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFPAASFVGNIVLALVLQRKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
EDSHPDLPGTEGGTEGKIVPSYDSATFP 508
                                                     EDSHPDLPGTEGGTEGKIVPSYDSATFP 398
                                                                                                                                            LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
                                                                                                                                                                                         LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGISESSVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LCSMTWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSPTHLFAFASVN
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                                                                                                                                                                                                                                                                                                                                                         -MNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV 310
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77.4%;
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Pred. No. 7.8e-202;
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The invention relates to isolated human G-protein coupled receptor (GCREC) polypeptides and their biologically active fragments. GCREC and protein is useful in treating a disease or condition associated with an increase or decrease in expression of functional GCREC. The GCREC's are useful in the diagnosis, treatment and prevention of cell proliferative disorders (cancer, leukaemia, melanoma); neurological disorders (stroke.

Claim 1; Page 125-126; 143pp;

English.

RESULT 12

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AAE15642
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22-JUN-2000; 2000US-215209P.
29-JUN-2000; 2000US-216595P.
14-JUL-2000; 2000US-218956P.
14-JUL-2000; 2000US-218956P.
19-JUL-2000; 2000US-218916P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; G-protein coupled receptor-12; GCREC-12; therapy; cancer; stroke; cell proliferative disorder; neurological; epilepsy; Parkinson's disease; Alzheimer's disease; alzheimer's disease; inflammation; thyroiditis; haemolytic anaemia; AlIS; Acquired Immune Deficiency Syndrome; dementia; nootropic; cholelithiasis; multiple sclerosis; atherosclerosis; angina pectoris; gastroenteritis; disheres.
                                                                                                               Isolated human G-protein coupled receptor polypeptides and the use of these sequences in the diagnosis, treatment and prevention of disease and in the assessment of exogenous compounds on the expression of the
                                                                                                                                                                                                              Griffin JA, Yue H,
Lu Y, Walia NK, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE15642 standard; Protein;
                                                                                                                                                                  N-PSDB; AAD24967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes; ulcer; viral infection; immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G-protein coupled receptor-12 (GCREC-12) protein
                                                                                                                                                                                                                                                               (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2001; 2001WO-US19275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                            2002-075627/10.
                                                                                                                                                                                                    VS,
                                                                                                                                                                                                                                     Baughn MR,
                                                                                                                                                                                                   Hernandez R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168..189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Mature_GCREC_12_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Signal_peptide
                                                                                                                                                                                                   R, Hafalia AJA, Nguyen DB,
Khan FA, Patterson C,
Graul R, Yao MG, Yang J,
nandez R, Walsh RT, Borows)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /labe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L= Signal_peptide
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                                                                                                                                                                                                    Borowsky ML,
                                                                                                                                                                                                            , Gandhi AR, Kallick D.
Lu DAM, Tribouley CM;
, Ramkumar J, Au-Young
                                                                                                                                                                                                    Thornton M,
                                                                                                                                                                                                   Au-Young
on M, He
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                                                                                                                                     attention deficit disorder; anxiety; depression; bipolar disorder; neurological disorder; Huntington's disease; dementia; chesity; and metabolic disorder; Parkinson's disease; Tourette's syndrome; through a disorder; and a disorder; myocardial infarction; or type 2 diabetes, cardiovascular disorder; myocardial infarction; or
                                                                                       type 2 diabetes, cardiovascular disorder; myocardial infarction; cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV; viral infection; immunostimulant; neuroleptic; nootropic; tranquili
                                                                                                                                                                                                                                                                                  Human G Protein-Coupled Receptor (GPCP) polypeptide #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                   18-DEC-2001
                                                                      antidepressant; anorectic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                        AAU25561 standard; Protein, 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           __
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLOCTHPYVYGYMRKTIKKEIQDMLKKFFCKEKPPVEDSHPDLFGTEGGTEGKIVPSYD 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLIVMIACYSVVFCAARPQHALLYNVFPHRLEVFVKDCVENEDEEGAEKKEEFQDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPISLAHSITASTVLVIFLANSFVSHIVLALVLAKFÇLLQVTHARFIFNLVTDILQISL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SATEP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCHESEVYAYEGEMEAYSSILKAYEGSTGTSESSVEARGSEEVRESSTVASSGSMEGYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TÖRRGYLLLYGTWIVAILQSTPFLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SATFP 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLQCCTHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYD 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STKVEENSMKADKGETEVNQCSIDLGEDDMEFGEDDINFSEDDVEAVNIPESLPPSRRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHFLSYPSK% 143
                                                                                                                                                                                                                                    G-protein coupled receptor; GPCR; mental disorder; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 AA;
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.8%;
77.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1901, DB 23
Fred. No. 3.2e-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                              neuroleptic; nootropic; tranquiliser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....MMIPESLPPSRRMS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                thrombosis;
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23.FEB.2000, 2000US-0194303.
23.FEB.2000, 2000US-0194305.
23.FEB.2000, 2000US-0194305.
23.FEB.2000, 2000US-0194307.
62.MAR.2000, 2000US-0196457.
63.MAR-2000, 2000US-018664.
13.MAR-2000, 2000US-0186864.
13.MAR-2000, 2000US-0188864.
13.MAR-2000, 2000US-0194344.
23.JUN 2000, 2000US-0194344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03 APR 2000; 2000US 0194344
23.JUN 2000; 2000US 0213861.
11.JUL-2000; 2000US 0217369.
11.JUL-2000; 2000US 0217369.
14.JUL-2000; 2000US 0218337.
20.JUL-2000; 2000US 0218327.
                                                                                                                                                                                                                                                                                                                                     Sequences AAU2554-AAU25616 represent human G-protein coupled receptor (GPCR) polypeptides of the invention. The proteins and their associated DNA sequences can be used to identify compounds which bind to GPCR polypeptides and in screening for compounds that modulate GPCR activity. By screening a human subject for the presence of mutations in GPCP DNA, a GPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, saxiety, depression, dementia and bipolar disorder, neurological disorders such as Huntington's disease, parkinson's disease and Tourette's syndrome, metabolic disorders such as chesity, ancrexia and type 2 diabetes, cardiovascular disorders such as thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis, viral infections caused by HIV and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid encoding a new G-protein coupled receptor polypeptide for detecting receptor modulators that can treat mental disorders, such as schizophrenia, anxiety, depression, or obesity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-AUG-2001.
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 35; Page 73; 279pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vogeli G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2001;
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   167
                                                                                                           51
                                                                                                                                               47
                                                                                                                                                                                                                                     Local
                                                                                                                                                                              1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
TIVVVSVDRYLSIIHELFYESKMTQREGYLLLYGTWIV 204
                                                                                            QLLQVTNEFIENLLVTDLLQISLVAPWVVATSVPLFWPINSHFCTALVSLTHLFAFASVN 120
                                                                                                                                            MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQPKP 106
                                  LIAAASADELTSIIHETSIBSHWEGEBSKTTTAGIMIA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-570628/64.
                                                                       QLLQVTNRF1FNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
                                                                                                                                                                                                                    157;
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS42813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood LS,
                                                                                                                                                                                                                                                                                          204 AA;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US05676
                                                                                                                                                                                                                                   37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parodi LA,
                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                   Score 794; DB 22;
Pred. No. 3.7e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lind
                                                                                                                                                                                                                                                      Length 204;
                                                                                                                                                                                                                     Indels
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Component length polymorphism (RFLP) associated with certain disorders, and including the capacity of cell as well as for genetic mapping. The nucleic acid is useful for the receptor, in the design of antisense and collustry of cells to expression of the expression of the expression of more to detect for the suppression of the expression of more and to cultured cell, tissue or an animal, for therapeutic purposes and to comprove a model for diseases of conditions characterised by aberrant receptor, it is also useful in hybridisation assays to detect the capacity of cells to express nGPCR-x, in diagnosis, to identify the monologues of nGPCR-x in other animals, for screening for restriction fragment length polymorphism (RFLP) associated with certain disorders, as well as for genetic mapping. The nucleic acid is useful in gene therapy. The nGPCR is useful as a research tool for identification, characterisation and purification of interacting, regulatory proteins. The antibody is useful for therapeutic and diagnostic purposes, and in cureat or prevent unregulated cellular growth, such as cancer mysoedema), renal failure, inflammatory conditions (e.g., Crohn's diseases), diseases enlated cellular growth, such as cancer diseases), diseases related to cell differentiation and homeostasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2000; 2000US-195093P.
06-APR-2000; 2000US-195098P.
06-APR-2000; 2000US-195198P.
06-APR-2000; 2000US-195150P.
06-APR-2000; 2000US-195151P.
06-APR-2000; 2000US-195151P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule encoding G protein-coupled receptor polypeptide, nGPCR-x, useful for treating cancer, Crohn's disease, rheumatoid arthritis, Alzheimer's disease, stroke, thrombosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleotide sequence that encodes a G protein-coupled receptor polypeptide, nGPCR-x, vectors and transformed cell expressing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 31; Page 80; 189pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metabolic disease; cardiovascular disease; type 2 diabetes; obesity; hypotension; hypotension; thrombosis; myocardial infarction; atherosclerosis; proliferative disease; hyperproliferative disorder; psoriasis; hormonal disorder; polycystic ovarian syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        central nervous system disorder; stroke; Huntington's disease; Tourette's syndrome; Parkinson's disease; Alzheimer's disease; viral infection; HIV-1; HIV-2; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; G protein-coupled receptor; nGPCR; cancer; tumour; thyroid disorder; myxoedema; renal failure; inflammatory condition; Crohn's disease; cell differentiation disease; homeostasis disease; rheumatoid arthritis; autoimmune disorder; movement disorder;
disease), diseases related to cell differentiation and homeostasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS62900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-010912/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001; 2001WO-US11330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alopecia; sexual dysfunction; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human G protein-coupled receptor from cDNA Seq-2644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to an isolated nucleic acid molecule comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
The present sequence represents histamine H2 receptor (H2RH) isolated from Incyte Clone 1722180 from the human bladder cDNA library (BLADNOT06). A host cell, comprising a vector which contains the nucleic acid encoding H2RH, can be used to produce the H2HR. An antibody which specifically binds the H2RH can be used to detect and quantify H2HR in a biological sample. An antagonist which specifically binds to and modulates the activity of H2RH can be used in a pharmaceutical composition for treating inflammatory disease, gastric conditions, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis, autoimmune disorders, movement disorders, central nervous system disorders (e.g., stroke, Huntington's disease, Tourette', Syndrome, Parkinson's disease, Alzheimer's disease), infections, such aviral infections caused by HIV-1 or HIV-2 (human immunodeficiency virus, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, hypotension, hypertension, thrombosis, myocardial infarction, atherosclerosis), proliferative diseases and cancers, hyperproliferative disorders (such as psoriasis), hormonal disorders (e.g., polycystic ovarian syndrome, alopecia), and sexual dysfunction. The present sequence represents an n-GPCR of the invention.
                                                                                                                                                                                 Claim 1; Page 51-52; 77pp; English.
                                                                                                                                                                                                                         conditions and nervous conditions
                                                                                                                                                                                                                                       Histamine H2 receptor - used to treat inflammatory disease, gastric
                                                                                                                                                                                                                                                                                   N-PSDB; AAV37701.
                                                                                                                                                                                                                                                                                                                                         Au-Young J, Goli SK,
                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9820040-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nervous condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; histamine H2 receptor; H2RH, inflammatory disease; gastric,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human histamine H2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW58586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW58586 standard; Protein; 454 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 PYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 PYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 NVKRHSLEVRVKDC---VENEDEEGAEKKEEFQDE----MNIPESLPPSRRNSNSNPPLP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 RCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SMKADKGRTEVNQCSIDLGEDDMEFGEDDINFSEDDVEAVNIPESLPPSRRNSNSNPPLP 63
                                                                                                                                                                                                                                                                                                      1998-286870/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIH 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AA;
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                                                                                                                                                                                                                                                                                                                                         Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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Pred. No. 1.8
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Best Local S
Matches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nervous conditions The gastric conditions that can be treated using the antagonist, include gastritis, flu, colitis, and Crohn's disease. The nervous conditions include Alzheimer's disease, ataxia, Eaton-Lambert syndrome, epilepsy, myasthenia gravis, and Parkinson's disease. The antagonist may also be used to treat infections or inflammation of the urinary tract and bladder. It may also be used to modulate HJHP activity in endothelial cells of the cardiovascular system and treat diseases such as arteriosclerosis, cardiomyopathy, endocarditis, and ischaemia.
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305
                                                                                                                                                   269
                                                                                                                                                                                                                                                                                               145 VMALVYIWLHSLIGCLPPLFGWSSVEFDEFKWMCVAAWHREPGYTAFWQIWCALFPFLVM 204
                                                                                                                                                                                                                                                                                                                               149 YLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVIPLIVM 208
                                                                                                 252 SRRNAFQGVVYSAN---
                                                                                                                                                                                                205 INCYGETERVÁR-----VKARKVHCGTVVIVEEDAQRTGVRKNS-----STSTSSSG 251
                                                                                                                                                                                                                                               100 IACYSVVECAARFOHALLYNVKPHSLEVRVKDCVENEDEEGAEKKEEFQDEMNIFESLPP 268
                                            SZU QVPQWVITIIIWHEELQUCIHPYVYGYMHKTIKKEIQDM 358
                                                                                                                                                                                                                                                                                                                                                                                                (J)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 GVIITQFIAIIVITIFVCLGNLVIVVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 GIIRSTVLVIFLAASFV--GNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
SLETWA----TWLSFASAVCHPLIYGLWNKTVRKELLGM 339
                                                                                                                                                                                                                                                                                                                                                                                                VTSSIRREWIFGVVWCNESALLYLLISSASMLTLGVIAIDRYYAVLYPMVYPMKITGNPA 144
                                                                                                                                                 SPRNS-----NSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY-CFLAVLAVW--VDVET 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                VATSVPLEWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 AA;
                                                                                              -QCKALITILVVLGAFMVTWGPYMVVIÅSEÅLWGKSSVSP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Mismatches 137; Indels 35; Gaps
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Search completed: February 11, 2003, 11:08:12 Job time: 86 secs

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Result
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1 MTSTCTNSTRESNSSHTCMP......GTEGGTEGKIVPSYDSATFP 398
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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  US-08-748-485-1
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US-09-030-582-2
PCT-US94-09051-2
US-08-34-698-6
US-08-468-939-6
US-08-468-939-6
US-08-468-534-6
US-08-468-534-6
US-08-722-130-6
US-08-722-130-6
US-09-206-899-6
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US-08-722-001-12
US-08-688-415-6
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11, Appl
11, Appl
23, Appl
23, Appl
23, Appl
17, Appl
17, Appl
17, Appl
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FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: BILINGS, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF 0159 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166 TELEX: INFORMATION FOR SEQ ID NO. 1: SEQUENCE CHARACTERISTICS: LENGTH: 454 amino acids TYPE: amino acids TYPE: amino acids TYPE: almino acids TYPE: almino acids STRANDEDNESS: single TOPOLOGY: linear INMEDIATE SOURCE: LIBRARY: Consensus CLONE: 1722180	US-08-748-485-1 US-08-748-485-1 US-08-748-485-1  Sequence 1, Application US/08748485  Patent No. 5817480  GENERAL INFORMATION: APPLICANT: Au-Young, Janice APPLICANT: Guegler, Karl J. APPLICANT: Guegler, Karl J. APPLICANT: Murry, Lynn E.  TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR NUMBER OF SEQUENCES: 8  CORRESPONDENCE ADDRESS: ADDRESSE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DESTATE: CA COUNTRY: Palo Alto STATE: CA COUNTRY: Palo Alto STATE: CA COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOCTWARE: FatESQ Version 2.0 CURRENT APPLICATION NUMBER: US/08/748,485 FILING DATE: Herewith CLASSIFICATION DATA: APPLICATION NUMBER:	28 326.5 15.6 572 1 US-08-334-698-2 29 326.5 15.6 572 1 US-08-228 932-2 30 326.5 15.6 572 1 US-08-468-939-2 31 326.5 15.6 572 1 US-08-468-939-2 31 326.5 15.6 572 1 US-08-722-001-30 32 326.5 15.6 572 2 US-08-722-190-2 34 326.5 15.6 572 2 US-08-722-190-2 35 326.5 15.6 572 2 US-08-244-354-2 36 326.5 15.6 572 3 US-09-268-999-2 37 326.5 15.6 572 3 US-09-268-415-2 38 326.5 15.6 572 4 US-09-444-783-2 39 324.5 15.6 572 4 US-09-484-15-2 39 324.5 15.5 422 1 US-08-117-920-3 41 324.5 15.5 422 1 US-08-117-920-3 42 324.5 15.5 422 1 US-08-117-06-3 43 324.5 15.5 422 1 US-08-216-594-3 44 324.5 15.5 422 1 US-08-117-06-3 45 324.5 15.5 422 1 US-08-15-13 46 324.5 15.5 422 1 US-08-117-056-3 47 324.5 15.5 422 1 US-08-117-056-3 48 324.5 15.5 422 1 US-08-117-056-3 49 324.5 15.5 422 1 US-08-117-056-3 49 324.5 15.5 422 1 US-08-117-056-3 40 324.5 15.5 422 1 US-08-117-056-3 41 324.5 15.5 422 1 US-08-118-13
		Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 30, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli

Query Match

20.6%;

Score 430.5;

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Length 454;

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; MOLECULE TYPE: protein US-08-467-568-2
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                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 29 2%; Pred. No 1 7e-30; Matches 99; Conservative 68; Mismatches 137; Indels
                                                                                                                                                                                                                                                        TELEFAX: 201-994-1744
INFOPMATION FOR SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTOPNEY/AGENT INFOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
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CITY: Roseland
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                                                                                                                                                                       TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER FILING DATE: 06-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
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                                         19.5%; Score 409; DB 2; Length 529; 28.5%; Pred. No. 1.3e-28; Indels tive 67; Mismatches 146; Indels
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                                             46; Gaps
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                                                                   MOLECULE TYPE:
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,582
                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                             NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,1
                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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Stewart & Olstein
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    Score 409;
Pred. No. 1
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RESULT 4
PCT-US94-09051-2
; Sequence 2, Application PC/TUS9409051
; GENERAL INFORMATION:
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CT-US94-09051-2
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                                                                                                                                   TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
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TITLE OF INVENTION: Add
NUMBER OF SEQUENCES: 2
COPPESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INC
                TOPOLOGY: L:
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PRIOR APPLICATION DATA:
                                                                                                                SEQUENCE CHARACTERISTICS:
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STREET: 6 BECK
CITY: ROSELAND
                                                                                                                                                                                                              NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-194
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                                                                        LENGTH: 529 AMINO ACIDS
TYPE: AMINO ACID
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                                                        STRANDEDNESS.
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E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
                                                                                                                                                      : 201-994-1700
201-994-1744
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US-08-334-698-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08334698 Patent No. 5556753 GENERAL INFORMATION:
                                      TELEX: (212) 422523 CC INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acid
                                                                                                                          REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                 TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 Rockefeller Plaza
466 amino acids
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US-08-228-932-6
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               ZIP: 10112
COMPUTER PEDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu, APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig TITLE OF INVENTION: USE OF ALPHA-IC SPECIFIC COMPOUNDS TO TPEAT BENIGN TITLE OF INVENTION: PROSTATIC HYPERPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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           TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
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TOPOLOGY: linear
                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                              APPLICATION NUMBER:
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Best Local Similarity
INFORMATION FOR SEQ ID NO:
                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNMBER: 28,678
REFERENCE/DOCKET NUMBER: 413:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 291-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:
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                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Y: U.S.A.
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                     Floppy disk
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RESULT 8
US-08-722-001-28
; Sequence 28, Application US/08722001
7-rent No. 5760054
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                 CLASSIFICATION: 514
PRIOP APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILLING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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  NAME:
                                                                                                                         FILING DATE:
                                                                                                                                          APPLICATION NUMBER:
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Lee, Hee-Yoon
Bell, Ian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thompson, Wayne J. Huff, Joel R.
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                                                                                                                                          US/08/722,001
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08406855A Patent No. 5861309
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
                 SOFTWARE: PatentIn Release #1.30 CURRENT APPLICATION DATA:
                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             ZIP: 10036
                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                          STATE:
                                                                                                                                                                                                              CITY: New York
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  APPLICATION NUMBER:
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US/08/406,855A
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US-08-722-190-6
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08722190 Patent No. 5990128 GENERAL INFORMATION.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 278-0400
TELEPAX. (212) 391 0526
INFORMATION FOR SEQ ITE NO. 6.
SEQUENCE CHARACTERISTICS:
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ATTORMEY/AGENT INFORMATION
NAME, White, John F.
                                                                                                                                                                                                                                                            APPLICANT: Charles Gluchowski, Carlos C. Forray, George APPLICANT. Chiu, Theresa A. Branchek, John M. Wetzel and Faul R. Hartig TITLE OF INVENTION. USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TITLE OF INVENTION. TREAT HENLOW FROSTATIC HYPERFLASIA NUMBER OF SEQUENCES. 6
CORPESPONDENCE ADDRESS:
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REFERENCE/COCKET NUMBER. 41
TELECOMMUNICATION INFORMATION.
                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CURRENT AFFLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 UK KERÇKEKPEKE-- DSHPDLEGTEGGTEGKI-VESTESATE 397
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                                                                                                                                 ZIP:
                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
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                                                               COMPUTER:
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                                                                                                                                 10036
                                                                                                                                                                          New York
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John F. 28,678
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                                                                                Floppy disk
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PEGISTRATION NUMBER 28,678
REFERENCE/SOCKET NUMBER 41
TELECOMMUNICATION IMPORMATION:
TELEPHONE: (212) 278-0400
TELEFAX. (212) 331-0525
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                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
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SOFTWARE.
                     COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               MEDIUM TYPE:
                                                                                                                                   COUNTRY:
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                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                       Charles Gluchowski, et al.
VENTION: USE OF ALPHA-10 STECTFIC COMPOUNDS
VENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
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US-09-206-899-6
                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09206899 Patent No. 6083705 GENERAL INFORMATION:
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                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 LPIQCLCPKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF 385
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17.7%; Score 371.5; DB 3; Length 466;
Local Similarity 26.9%; Pred. No. 2.5e-25;
hes 109; Conservative 77; Mismatches 180; Indels 39;
                                                                                ZIP:
                                                                                                                                            STREET:
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                                                                                                 COUNTRY:
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FILING DATE: April 1, 1997
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         STATE:
                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                10036
                                                                                                                                            New York
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                                                                                                   New York
                                                                                                                                                              E: Cooper & Dunham LLP
1185 Avenue of the Americas
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Jonathan A. Bard et al.
VENTION: DNA Encoding Human Alpha 1 Adrenergic
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                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                       Sequence 6, Application US/09444783 Patent No. 6420389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
COMPUTER READABLE FORM
                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1 30 CURRENT APPLICATION DATA:
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               21P:
                                                         CITY:
STATE:
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                                                                              STREET: 1185 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122
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                                   COUNTRY
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                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                  Charles Gluchowski, et al.
VENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS
VENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
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                                                                                                                      COOPER & DUNHAM LLP
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OPERATING SYSTEM: PC-DOS/MS-DOS

MEDIUM TYPE: COMPUTER: I

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US-09-688-415-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09688415
Patent No. 6448011
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                                                                                                                                                                                                               APPLICANT: Bard, Jonathan A
APPLICANT: Forray, Carlos
APPLICANT: Weinshank, Richard L
TITLE OF INVENTION: DNA ENCOPING HTMAN ALPHA: APPENEEGIC PECEFTOFS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 41337aza
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Best Local :
                            FILE REFERENCE: 41337aza
CURRENT APPLICATION WIMPEP: US/09/688,415
CUPPENT FILING DATE: 2000-10-16
PRIOR APPLICATION WIMPER: 09/474,551
PRIOR FILING DATE: 1099-10-09
NUMBER OF SEQ ID NOS:
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LENGTH: 466 amino acid
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ATTORNEY/AGENT INFORMATION
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CURPENT APPLICATION DATA
APPLICATION NUMBER: US/09/444,78
FILING DATE:
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VER: 28,678
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GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carles C. Forray, George APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and TITLE OF INVENTION. USE OF ALPHA-1C SPECIFIC COMPONING.
TITLE OF INVENTION. TREAT BENIGN PROSTATIC HYPERPLASIA.
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Rest Local Similarity
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                         ATTOPHEY/AGENT INFORMATION NAME: White, John PREGISTRATION NUMBER. 28,
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: COOPER & DUNHAM LLP
                                                                                                                                                                                                                                                 CUPPENT APPLICATION DATA:
                                        PREFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0409
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TELEFAX:
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SOFTWARE: PatentI
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                                                                                                                                                                                                                            APPLICATION NUMBER:
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                     (212) 391-0525
                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                       IBM PC
                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                         4-APR-1995
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26 9%; Fred No 2.5e 25;
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                                                                                                              28,678
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                                                                     341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGOHKDMVRIPVGSRETF 385
                                                                                                          359 LK-KFFCKEKPPKE----DSHPDLPGTEGGTEGKI-VPSYDSATF 397
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                                                                                                                                                                                            299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
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TYPE: amino acid
TOPOLOGY: linear
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Maximum DB seq length: 2000000000
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/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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1: /cgn2_6/ptodata/2/pubpaa
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	2024	96.7	508	y i	US-09-791-932-112	1
2	794		204	ω	US-09-791-932-68	717
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4	409		UT I	10	115-04-421-8-5	sequence 115, App
υı	371.5	17.7	466	۱ ۵	TIS=10-185-881 6	sequence 2, Appli
	366.5	17.5	466	10	15-09-951-802-17	sequence 6, Appli
7	326.5	15.6	501	10	US-09-951-622-4	1
	326.5		572	9	US-10-185-991-2	
	324.5		422	9	US-10-166-101-3	,
10	321		451	10	US-09-993-844-6	ב
11	319		497	12	US-10-052-589-2	•
12	319		517	10	US-09-951-622-10	, ,
13	319	15.2	520	9	US-10-185-991-4	۲ د
14	299	14.3	259	φ	JS-10-080-960-25	ب - ۱
15	299	14.3	259	9	US-10-012-140-27	) L
16	299	14.3	259	9	JS-10-012-140-29	) i
17	299	14.3	259	9	US-10-077-698-3	, ,
18	299	14.3	259	10	US-09-796-338A-23	7,72
19	297	14.2	445	10	US-09-989-861-16	Sequence 16, Appl

## ALIGNMENTS

US-09-791-932-112; Ag; Sequence 112, Ag; Publication No.

Application US/09791932 o. US20030003451A1

; GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Lind, Peter

Vogeli, Gabriel Parodi, Luis A. Hiebsch, Ronald R.

APPLICANT: APPLICANT: RESULT 1

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PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184
PRIOR APPLICATION NUMBER: 60/184
PRIOR APPLICATION NUMBER: 60/184
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/791,932
CURRENT FILING DATE: 2001-02-23
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                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linda S.
N: No. US20030003451Alel G Protein-Coupled Receptors Cross-Reference
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RESULT 2
US-09-791-932-68
; Sequence 68, Application US/09791932
; Publication No. US20030003451A1
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; CRGANISM: Homo sapiens
US-09-791-932-112
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CUPPENT APPLICATION NUMBER: US/09/791,932
TIPPENT FILING DATE: 2001-02-23
PRIOP APPLICATION NUMBER: 60/184,305
PRIOP FILING PATE: 2000 02-23
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                                                                      TITLE OF INVENTION: No. US20030003451A1el FILE REFERENCE: 00325 US1
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PRIOR FILING DATE: 2000-
NUMBER OF SEQ ID NOS: 18
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Ruff, Valerie
Huff, Rita M.
Wood, Linda S.
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Parodi, Luis A.
Hiebsch, Ponald P.
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                                                                                                                                                              Paul S.
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                                                                                     Protein-Coupled Receptors Cross-Referen
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                                                                                                                                                                                                                                                  Sequence 115, Application US/09828644
Fatent No. US20020015998A1
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/828,644
CURRENT FILING DATE: 2001-04-06
                                             PRIOR APPLICATION NUMBER: 60/195,099
PRIOR FILING DATE: 2000-04-06
PPIOP APPLICATION NUMBER: 60/195,151
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,148
                                                                                                                                                                                                    TITLE OF INVENTION: No. US20020015998A1el G Protein-Coupled Receptors FILE REFERENCE: 00196US1
                                                                                                                                                                                                                                     APPLICANT: Vogeli, Gabriel
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,093
PRIOR FILING DATE: 2000-04-06
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99.4%;
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Pred. No. 4.4e-65;
0; Mismatches 1
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; TYPE: PRT
; ORGANISM: human
US-09-951-622-2
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TITLE OF INVENTION: ADRENERGIC RECEPTOR
FILE REFERENCE: PF128D2C1
CURRENT APPLICATION NUMBER: US/09/951,622
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/39,244
PRIOR FILING DATE: 1999-06-24
PRIOR PPLICATION NUMBER: 09/030,582
PRIOR APPLICATION NUMBER: 09/030,582
PRIOR APPLICATION NUMBER: 09/467,568
PRIOR APPLICATION NUMBER: 08/467,568
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR PILING DATE: 1995-08-06
PRIOR PILING DATE: 1994-08-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
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US-09-951-622-2
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Patent No. US20020106734A1
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LENGTH: 242
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PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/230,149
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin version 3.0
181 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARROHALLYNVKRHSLEVRVKD 249
                                                                     117 TLGÝTAIDŘÝYAVLYÞMVÝÞMKITGNŘAVMALVYIЙLHSLIGCLÞÞÍÞGMSSVEYGÉNKW 176
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                                                                                                               121 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA 180
                                                                                                                                                           57 YLLTLSNKFVFSLTLSNFLLSVLVLÞFVVTSSIRREWIFGVVWCNFSALLYLLISSASML 116
                                                                                                                                                                                                          61 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 PYVYGYMHKTIKKEIQDMLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 NVKRHSLEVRVKDC----VENEDEEGAEKKEEFQDE----MIPESLPPSRRNSNSNPPLP 280
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                 6 TNSTRE-----SNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP 60
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36.8%; Score 769.5; DB 10; Length 242;
Local Similarity 81.5%; Pred. No. 9.4e-63;
nes 145; Conservative 7; Mismatches 19; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SMKADKGRTEVNQCSIDLGEDDMEFGEDDINFSEDDVEAVNIPESLPPSRRNSNSNPPLP 63
                                                                                                                                                                                                                                                                                                                                                               103; Conservative
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INFORMATION FOR SEQ ID NO: 6:
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128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
                                               63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122
                                                                                                                                                                                                                   / Match 17.7%; Score 371.5; DB 9; Length 466; Local Similarity 26.9%; Pred. No. 4.1e-26; Local Similarity 77; Mismatches 180; Indels 39; Gaps
                                                                                       68 RFIFNLLVTDLLOISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
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                                                                                                                                     5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62
                                                                                                                                                                               8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
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                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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FILING DATE: 28-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: USE OF ALPHA-IC SPECIFIC COMPOUNDS
TREAT BENIGN PROSTATIC HYPERPLASIA
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                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 466 amino acids
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TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.24
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US-09-951-622 11
Sequence 11, Application US/09951622
Patent No. US20020106734A1
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TITLE OF INVENTION: ADDENERGIC PECEPTOR
FILE REFERENCE: P128B2C1
CUPPENT FILING DATE: 2001-09-14
PPIOP APPLICATION NUMBER: 09/339,244
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR PRILICATION NUMBER: 09/467,568
PPIOP APPLICATION NUMBER: 09/467,568
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PPIOP APPLICATION NUMBER: 09/467,568
PPIOP PILING DATE: 1994-08-10
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ORGANISM: human
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                                                                              299 VLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
                                                                                                                                                                                                                                                                                                                                                                      123 DPYTGVSYPLPYPTTVTQPRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179
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                                                                                                                                                                                                                                                                                                                                                                                                                          128 DPYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 17.5%, Score 366.5, DB 10, Length 466; Local Similarity 26.7%; Pred. No. 1.2e-25; hes 109; Conservative 76; Mismatches 182; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 PETENILIVTDILIQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
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                        VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340
                                                                                                                                                                                                NEDEEG----AEKKEEFQDEMNIPESLPPSPRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
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US-09-951-622-9
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LENGTH: 501
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Patent No. US20020106734A1
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CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/339,244
PRIOR FILING DATE: 1999-06-24
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PRIOR FILING DATE: 1998.02-25
PRIOR APPLICATION NUMBER: 08/467,568
PRIOR FILING DATE: 1995-06-06
PRIOR PRIOR PRIOR NUMBER: PCT/US94/09051
PRIOR FILING DATE: 1994-08-10
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                                                                             IDIICATIO: WO. TO GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION. USE OF ALPHA-1C SPECIFIC COMPOUNDS
TITLE OF INVENTION. TREAT BENIGN PROSTATIC HYPERPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
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RESULT 9
JS-10-166-101-3
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                                                                                                                                        Sequence 3, Application US/10166101 Publication No. US20030008823A1 GENERAL INFORMATION:
         APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul
TITLE OF INVENTION: DNA Encoding A 5-HTIF Receptor And Uses Thereof
FILE REFERENCE: 39218-c
CURRENT APPLICATION NUMBER: US/10/166,101
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INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                373 LFPQLKPSEGVFKVIFWLGYFNSCVNPLIYPCSSREFKRAFLRLLR 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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FILING DATE: 28-Jun-2002
CLASSIFICATION: <Unknown>
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TELEFAX: (212) 391-0525
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APPLICANT: Oakley, Robert H.
APPLICANT: Barak, Lawrence S.
APPLICANT: Barak, Lawrence S.
APPLICANT: Laporte, Stephane A.
APPLICANT: Laporte, Stephane A.
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Modified G-Protein Coupled Receptors
FILE REFERENCE: 033072-026
CURRENT APPLICATION NUMBER: US/09/993,844
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,772
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
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US-09-993-844-6
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                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09993844 Patent No. US20020106739A1
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SEQ ID NO 3
LENGTH: 422
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Best Local Similarity
LENGTH: 451
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PRIOR FILING DATE: 1992-01-08
NUMBER OF SEQ ID NOS: 13
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PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 08/483,222
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/117,006
PRIOR FILING DATE: 1994-08-22
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PRIOR FILING DATE: 1993-01-08
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Best Lucal Cir
Matches 100,
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Patent N., US2002013832A1

JENERAL INFORMATION.

APPLICANT. Ferez, Dianne
APPLICANT. Zuscik, Michael
TITUE OF INVERTION. Model Systems for neurodogenerative and cardiovascular disorders
FILE REPREPAISE 26473/94260
CURPENT APPLICATION NUMBER US/10/052,589
CURRENT FILING DATE. 2000-05-10
PRIOR APPLICATION NUMBER US 09/568,255
PRIOR APPLICATION NUMBER US 09/568,255
PRIOR FILING CARE. 2000-05-10
NUMBER OF SEQ ID NOS. 3
                                                                                              Matches
                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 497
                                                                                                                       Query Match
Best Local :
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ORGANISM: Artificial Sequence
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ORGANISM: Mesocricetus sp.
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32 DENSTLEQUIVERAISVGL....VLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87
                                               14 SSHTCMFLSKMFISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKFQLLQVTNRFIFNL 73
                                                                                           Mutch 15.2%; Score 319, DB 12, Length 497;
Local Similarity 26.0%, Pred. No. 2.7e-21,
Nes 92, Conservative 70; Mismatches 162; Indels 3;
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Patent No. US20020106734A1
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Best Local :
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CURPENT APPLICATION NUMBER: US/00/951,622
CURPENT FILING DATE 2001-09-14
PRIOR APPLICATION NUMBER: 09/339,244
PRIOR FILING DATE: 1909 06 24
PRIOR FILING DATE: 1909 06 24
PRIOR APPLICATION NUMBER: 09/030,582
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PRIOR FILING DATE: 1994-08-10
NUMBER OF SEQ ID NOS: 13
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TITLE OF INVENTION: ADPENEPGIC PECEPTOP
FILE REFERENCE: FF128D2C1
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PRIOR APPLICATION NUMBER: 08/467,568
PRIOR FILING DATE: 1995-06-06
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306 CFLAVLAVWVDVETQVFLWVITTIIWLFFLCOSHFFYVYSYMHETIEE 353
                                                                                                                                                                                 502
                                                                                                                                                                                                                                                                                 148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEFAPND-DKECGVT--EEPFYA 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 CFLAVLAVWVDVETOVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKETQDML 359
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                                                                                                                                                                                                                                                                                                                                  134 IHPLSYPSKMTORRGYLLLYGTWIVAILOSTPPLYGWGQAAFDERNALGSMIWGASPSYT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 SSHTCMPLSEMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
hes 92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       98 AMADLLLSFTVLPFSAALEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                        74 LVTDLIQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 ŚŚNSTLP. - QUDITRAISVGLVLGAFILFAIVĠNILVILSVACNEHLETPTNYFIVNL 87
                                                                                                                                                                                                                                 ILSVVSFIVIELIVMIACYSVVFCMAREQHALL....
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                                                                             DTLSSTFAKGHNPRSSIAVKLFFFSREK-----
                                                                                                                           DEEGAEKKEEFQDEMNIPESLPPSPRINSNSNPPLPFCYQCKAAKVIFIIIFSYVLSIGPY 305
                                                                                                                                                                           LESSIGSFYIDLAVILVMYCFVYIVAKETTRALEAGVMKEMSNGFELTLFIHSKNF HE
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26.4%, Fred. Mo. 2 8e 21;
ative 66; Mismatches 160; Indels 3
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                                                                                ----KAAKTLGIVVGMFILCWLPF
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; Sequence 4, Application US/10185991
; Publication No. US20030022900A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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INFORMATION FOR SEQ ID NO: 4:
306 CFLAVLAVMVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKK 353
                                                  263 DTLSSTKAKGHNPRSSIAVKLFKFSREK--
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APPLICANT: Char
                                                                                   246 DEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY 305
                                                                                                                              205 LFSSLGSFYÍÞLAVILVMÝCRVYIVÁKRTTKNÍEAGVMKEMSNSKELTÍRIHSKNF--HE 262
                                                                                                                                                                         194 ILSVVSFIVIPLIVMIACYSVVFCAARROHALL-----YNVKRHSLEVRVKDCVENE 245
                                                                                                                                                                                                                     148 RYSLQYPTLVTRRKAILALLSVWVLSTVIŠIGPLLGWKEPAPND-DKECGVT--EEPFYA 204
                                                                                                                                                                                                                                                             134 IHPLSYPSKMTORRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
                                                                                                                                                                                                                                                                                                             88 AMADLILSFTVLPFSAALEVIGYWVLGRIFCDIWAAVDVLCCTÄSILSLCAISIDRYIGV 147
                                                                                                                                                                                                                                                                                                                                                      74 LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
                                                                                                                                                                                                                                                                                                                                                                                                   32 ŚŚNSTLĖ----QLDITRAISVGLVĹGAĖILFAIVĠNILVILSVACNRHLRTPTNYĖIVNL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                            14 SSHTCMPLSKMPISLAHGIIRSTYLVIFLAASFYGNIVLALVLQRKPQLLQVTNRFIFNL 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/444,783
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TREAT BENIGN PROSTATIC HYPERPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/185,991
FILING DATE: 28-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.2%; Score 319; DB 9; Length 520; 26.4%; Pred. No. 2.8e-21;
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                                             -----KAAKTLGIVVGMFILCWLPF 310
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US-10-012-140-27

Sequence 27, Application US/10012140

Publication No. US20030009017A1

GENERAL INFORMATION:

APPLICANT: Leiby, Kevin R.

APPLICANT: Kapeller-Libermann, Rosana

APPLICANT: Glucksmann, Maria A.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 259
TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Publication No. US20020197695A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
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TITLE OF INVENTION: 80090, 52874,52880,63497, AND 33425
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF FILE REFERENCE: 38155-20044.00
CURRENT APPLICATION NUMBER: US/10/080,960
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,040
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,637
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                               318 ETQVPQWVITIIIWLFFLQCCIHPYVY 344
                                                                                                                                                                                                                                                                                                                                                                                                                     267 PPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY-----CFLAVLAVWVDV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 VILVĆYTRILRTLR-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PPLLFSWVKTVEEGNGTLNVNVTVCLIDFPEESTASVSTW--LRSYVLLSTLVGFLLPLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 PP-LYGWGQAA------FDERNALCSMIWGASPSYTILSVVSFIVIPLI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 ALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQ-RRGYLLLYGTWIVAILQST 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LVTALDVVNMYASILLLTAISIDRYLAIVHÞLRYRRRRTSPRRAKVVILLVMVLÁLLLSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          local Similarity
les 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     -KAAKTLLVVVVVFVLCWLPYFIVLLLDTLCLSIIMSSTCEL 233
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Search completed: Fobritary 11, 2003, 11:11:37 Job time : 15 secs
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LENGTH: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 VMIACYSVVFCAARRQHALLYNVKRHSLEVRVKDCVENEDEEGAEKKEEFQDEMNIFESL 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PPLLFSWVKTVEEGNGTLNVNVTVCLIDFPEESTASVSTW--LPSYVLLSTLVGFLLPLL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 FP-LYGWGQAA------FDERNALCSMIWGASPSYTILSVVSFIVIPLI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 ALVSLTHLEAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQ-RRGYLLLYGTWIVAILQST 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 PESRKNSNSNEELEKCYQCKAAKVIFIIIFSYVLSLGPY------CFLAVLAVWVDV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LVTALDVVNMYASILLLTAISIDRYLAIVHPLRYRRRRTSPRPAKVVILLVWVLALLLSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETOVPOWVITIIIWLFFLOCCIHPYVY 344
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Result
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Maximum DB seq length: 2000000000
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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
265.5	266	266.5	267.5	268.5	268.5	269	269	270	271	271	271	271.5	272.5	273	273.5
12.7	12.7	12.7	12.8	12.8	12.8	12.9	12.9	12.9	12.9	12.9	12.9	13.0	13.0	13.0	13.1
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I51666	I50475	DYHUD1	QRHUB2	A43956	A53281	S10127	QRHUB1	T15941	S36794	S08146	DYMSD2	C29514	I53040	S33776	DYBOD2
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Experimental source: cardiac myocyte c;Comment: This factor comprises a multigene family. As do alpha-2 and beta-adrenergic rec;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-38, /L',40-66, 'G',68-466 <REZ>,
A;Cross-references: EMBL:U1368; NID:g555851; PIDN:AAA52103.1; PID:g555852
R;Rokosh, D.G.; Bailey, B.A.; Stewart, A.F.R.; Karns, L.R.; Long, C.S.; Simpson, P.C. Biochem. Biophys. Res. Commun. 200, 1177-1184, 1994
A;Title: Distribution of alpha 1C-adrenergic receptor mRNA in adult rat tissues by RNase A;Reference number: PC2179; MUID:94241969; PMID:8185565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;26-42/Domain: transmembrane #status predicted <TM1>F;73-89/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: neurotransmitter receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 102-279 < ROK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U07126; NID:g595275; PIDN:AAA62866.1; PID:g595276
R;Stewart, A.F.; Rokosh, D.G.; Bailey, B.A.; Karns, L.R.; Chang, K.C.; Long, C.S.; Kariya; Circ. Res. 75, 796-802, 1994
A;Title: Cloning of the rat alpha 1C-adrenergic receptor from cardiac myocytes. alpha 1C, A;Reference number: I52862; MUID:95008062; PMID:7923624
A;Accession: I52862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-1C adrenergic receptor - rat (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (CDate: 02-Aug-196 #sequence revision 02-Aug-1996 #text_change 20-Apr-2000 (CACCESSION: I57959; I52862; FC2179 R.Haz, T.M.; FORTAY, C.; Smith, K.E.; Bard, J.A.; Vaysse, P.J.; Branchek, T.A.; Weinshan, Mol. Pharmacol. 46, 414-422, 194 A.; Title: The rat homologue of the bovine alpha 1c-adrenergic receptor shows the pharmacol A; Reference number: I57959; MUID:95021119; PMID:7935320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: PC2179
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                                                                                                                                                                                                                                                          Matches 106;
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67 NRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
                                                                                                                                                                                                                                                                                                    Local
                                                                           7 NASEGSNCTH-----PPAPVNISKAILLGVILGGLIIFGVLGNILVILSVACHRHLHSVT 61
                                                                                                                                                  7 NSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
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hypothetical prote

serotonin receptor serotonin receptor serotonin receptor adenosine receptor serotonin receptor

muscarinic acetylc

dopamine receptor

13.6 13.6 13.4

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submitted to the EMBL Data Library, July 1994
A;Reference number: 865656
A;Accession: 865656
A;Accession: 865656
A;Accession: 865656
A;Molecule type: mRNA
A;Residues: 1-429 *TAN>
A;Cross references: EMBL:D32201, NID.g927210; PIDN.BAA06900.1; PID.g927211
P;Hirasawa, A; Shibata, K; Herie, F; Takei, Y; Chika, K; Tanaka, T.; Muramoto, N.;
FEBS Lett. 363, 256-260, 1905
A;Title: Cloning, functional expression and tissue distribution of human alpha(IC)-adren
A;Reference number: 865654; MUID:95255557; FMID:7737411
A;Accession: 865654
A;Molecule type: mRNA
A;Residues: 424-429 *HIR>
A;Cross-references: EMBL:D32201
C;Genetics:
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865656

865656

Alpha-IC-adrenergic receptor splice form 3 - human alpha-IC-adrenes: alpha-IC-adrenoceptor isoform 3 C.Species: Homo sapiens (man)

C.Date: 22 Nov-1996 #sequence_revision 22 Nov-1996 C.Accession: 865656; 865654

R.Tanaka, T.
   Db
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Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_charge 20-Jun-2000
                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281
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180 EEPGYVLFSALGSFYLPLAIILVMYCPVYVVAKPESPGLKSGLFTDFSDSEQVTLRIHRK 239
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                                                                                                                                                                                                                                                                   6) YYIVNIAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122
                                                                                                                                                                                                                                                                                                                                          8
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                                                               ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
                                                                                                                                                                                                                                                                                                                                   REIENLLVTDLLQISLVAPWVVATSVPLFWPLNSHECTALVSLTHLFAFASVNTIVVVSV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVLSTGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRO----HALLYNVKRHSLEVRVKDCV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDRYIGVSYPLRYPTIVTORROVRALLOVWVLSLVISIGPLFGWFQPA-PEDETICGI-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMGLCIIS 121
                                                                                                                              DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179
                                                                                                                                                                                                 DPYLSTIHPLSYPSKMTORRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
                                                                                                                                                                                                                                                                                                                                                                                                     SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENEDEEG....AEKKEEFQDEMMIDESLPPSRRNSNSNPPLFRCYQCKAAKVIFIIIFS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEEPGYVLFSALGSFYVPLAIILVMYCPVYVVAKPESPGLKSGLKTDKSDSEQVTLPIHP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDRYLSTIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNVPAEGGGVSSAKNKTHFSVRL-----LKFSREK------KAAKTLGIVVGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.5%; Score 366.5; DB 2 26.7%; Fred. No. 2.8e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76; Mismatches 182; Indels
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Matches 108;

Conservative

76;

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Indels

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F;101-122/Domain: transmembrane #status predicted <TM3>F;144-165/Domain: transmembrane #status predicted <TM4>F;183-205/Domain: transmembrane #status predicted <TM5>F;183-298/Domain: transmembrane #status predicted <TM6>F;274-298/Domain: transmembrane #status predicted <TM7>F;7,13,22/Binding site: carbohydrate (Asn) (covalent) #s
                                                                                                                                                                                                                                                                                                                                    C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; glycoprotein; receptor; transmembrane
F;26-51/Domain: transmembrane #status predicted <TM1>
F;66-90/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 202-344 ¢DIE>
A;Residues: 202-348 ¢DIE>
A;Cross-references: GB.S76001; NID:g913817; PIDN:AAD14205.1, PID:g4261905
A;Cross-references: GB.S76001; NID:g913817; PIDN:AAD14205.1, PID:g4261905
R;Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.; & Blochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A;Title: Cloning, expression and characterization of human alpha adrenergic receptors alf
A;Peference number: JC2331; MTID:g4296492; FMID:8024574
A;Accession: JC2333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:L31774; NID:g666892; PIDN:AAB59486.1; PID:g666893 R;Diehl, N.L.; Shreeve, S.M.
Eur. J. Pharmacol. 268, 393-398, 1994
A;Title: Identification of the alpha 1c adrenoceptor in rabbit arteries & A;Reference number: I47013; MUID:95104335; PMID:7805763
A;Accession: I84635
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 296-346,'C',348-430,'Q',432-466 <ELL>
A;Cross-references: EMBL:U08994; NID:g497243, PIDN:AAA18783.1; PID:g497244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-130,'F',132-140,'P',142-166,'C',168-247,'H',249-337,'C',339-430,'Q',432-466
A;Crcss-references: GB:S70782; NID:3547219; FIDN:AAR31163.1, FID gf47220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: ADRAIC; ADRAIL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: G06938
A; Accession: G01419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Elliston, K.O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 295/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, April 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Comment: This protein plays critical roles in the regulation of a variety of physiolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRFNSNSNPPLFPCYQCKAAKVIFIIIFSY 298
   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRIQCLRRKQSSKHALGYTLHPPSQAVEGQHKDMVRIPVGSRETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAPAGGSGMASAKTKTHFSVRL-----LKFSREK------KAAKTLGIVVGCF 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-466 <HIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8p21-8p11.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDB:128088; OMIM:104221
   17.5%; Score 366.5, 26.7%; Pred. No. 3.
                                                                                                                  (covalent) #status predicted
3.1e-23;
                                   DB 2;
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C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; neurotransmitter receptor
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A;Cross-references: GDB·128088; OMIM:104221
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A;Residues: 424-499 <HIR>
A;Cross-references: EMBL:D32202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Tille: Cloning, functional expression and tissue distribution of human alpha(1C)-adrerA;Reference number: $65654; MUID:95255557; PMID:7737411
A;Accession: $65655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:D32202; NID:g927208; PIDN:BAA06901.1; PID:g927209 R;Hitasawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Obika, K.; Tanaka, T.; Muramoto, N.; FEBS Lett. 363, 256-260, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 20-Jun-2000
C;Accession: S65657; S65655
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A; Residues: 1-499 < TAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, July 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-1C-adrenergic receptor splice form 2 - human N;Alternate names: alpha-1C-adrenoceptor isoform 2
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A;Accession: S65657
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                                                                                                                                                                                                                                                                                                                                                             Query Match
128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
                                                                                63 YYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISI 122
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                                                                                                                                  68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 LKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 NEDEEG-----AEKKEEFQDEWNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 EEFGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCVE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 DRYIGVSYPLRYPTIVTORRGLMALLCVWALSLVISIGPLFGWROPA-PEDETICOI--N 179
                                                                                                                                                                                    5 SGNASDSSNCTQP--PAPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVTH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187
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                                                                                                                                                                                                                                     STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTN 67
                                                                                                                                                                                                                                                                                                     108; Conservative
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                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                              17.5%; Score 366.5; DB 2; Length 499; 26.7%; Pred. No. 3.3e-23;
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-1-adrenergic receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-466 < SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Schwinn, D.A.; Lomasney, J.W.; Lorenz, W.; Szklut, P.J.; Fremeau Jr., R.T.; Yang-Feng, J. Biol. Chem. 265, 8183-8189, 1990
A;Title: Molecular cloning and expression of the cDNA for a novel alpha-1-adrenergic receasion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
400 FSS 402
                                                                                340 VLRIQCLRRKQSSKHTLGYTLHAPSHVLEGQHKDLVRIPVGSAETFYKISKTDGVCEWKI 399
                                                    389 VPS 391
                                                                                                                                  358 MIKKFFCKEKPPK------EDSHPDL-----PGTEGGTEGKI 388
                                                                                                                                                                                    281 FVÍCWLÞF-FLVMÞIGSFFÞDERÞSETVFKÍAFWÍGYLNSCÍNÞITYÞCSSQEFKKAFON 339
                                                                                                                                                                                                                                      298 YVLSLGPYCFLAVLAVMVDVETQVPQMVITIIIMLFFLQCCIHPYVYGYMHKTIKKEIQD 357
                                                                                                                                                                                                                                                                                                 239 KNAQVGGSGVTSAKNKTHFSVRL----LKFSREK--
                                                                                                                                                                                                                                                                                                                                           243 ENEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS 297
                                                                                                                                                                                                                                                                                                                                                                                             179 NEEPGYVLFSALGSFYVPLTIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                               187 GASPSYTTLSVVSFTVIPLIVMIACYSVVFCAARRQ----HALLYNVKRHSLEVRVKDCV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 VDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIW 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 HYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNVWAAVDVLCCTASIMGLCIIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 NRFIFNLLVTDLLQISLVAFWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 LRIQCLRRKQSSKHALGYTLHPPSQAVEGOHKDMVRIPVGSRETF 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 LKKFFCKEKPPKEDS-----HPDLPGTEGGTEGKI-VPSYDSATF 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 VLCWLPF-FLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFQNV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 NAPAGGSGMASÄKTKTHÉSVRL----LKFŚREK-----KAAKTLGÍVVGCF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 VISLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 NEDEEG-----AEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSY 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 BEPGYVLFSALGSFYLPLATILVMYCRVYVVAKRESRGLKSGLKTDKSDSFQVTLRIHRK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQ----HALLYNVKPHSLEVRVKDCVE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 DRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWRQPA-PEDETICQI--N 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 NASDSSNCTH-----PPPPVNISKAILLGVILGGLILFGVLGNILVILSVACHRHLHSVT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 NSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.0%; Score 356.5; DB 2; Length 466; 25.5%; Pred. No. 2.1e-22; tive 74; Mismatches 176; Indels 65; Gaps
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R;Albert, P.R.; Zhou, Q.Y.; Van Tol, H.H.M.; Bunzow, J.R.; Civelli, O.J. Biol. Chem. 265, 5825-5832, 1990
A;Title: Cloning, functional expression, and mRNA tissue distribution A;Peference number: A35181; MUID:90202832; PMID:2156831
                                                                                                                                                                                                                                                                                                                C;Date: 12 Feb 1993 #sequence revision 12 Feb-1993 #text_change 13-Aug-1993 C;Accession: JH0315; A35181  
C;Accession: JH0315; A35181  
R;Fujiwara, Y; Nelson, D.L.; Kashihara, K.; Varga, E.; Roeske, W R.; Yamamura, H.I. Life Sci. 47, 127-132, 1990  
A;Title: The cloning and sequence analysis of the rat serotonin-1A receptor gene. A;Peference number: JH0315; MJID:90355775; PMID:2167416
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <YAS>
A;Cross references: EMBL:D63859
A;Cross references: EMBL:D63859
A;Note if is uncertain whether Met-1 or Met-8 is the initiator C;Superfamily: vertebrate rhodopsin
A;Accession: A35181
A;Molecule type: DNA
A;Residues: 1-372,'S',374-422 <ALB>
A;Cross-references: GB.J05276, NID.
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-422 < F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   serotonin receptor 1A - rat
N;Alternate names: 5-hydroxytryptamine receptor 1A (5-HTR1A)
C;Species: Rattus norvegicus (Norway rat)
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Eur. J. Blochem. 235, 501-507, 1996
A;Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Ma
A;Reference number: S71323; MUID:96184522; PMID:8654394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Oryzias latipes (Japanese medaka)
Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 SNCSHVLAP----ELNTVKAVVLGMVLGIFILFGVIGNILVILSVVCHEHLQTVTYYFIV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 SNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQPKPQLLQVTNPFIF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AHHH-HLSVGQSQTQGHSLTISLDSKGAP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDSHPDLPGTEGGTEG-KIVPSYDSATFP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVWVDVETQVP-QWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKEEFODEMNIPESLPPSPPNSNSNPPLPPCYQCKAAKVIFIIIFSYVLSLGPYCFLAVL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVSYPLRYPAIMTKPPALLAVMLLWVLSVIISIGPLFGWKEPA-PEDETVCKIT--EEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIIHPLSYPSKMTQPRGYLLLYGTWIVAILQSTPFLYGWGQAAFDERNALGSMIWGASPS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVERYL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIGSIFPAYRPSDTVFKITFWLGYFNSCINPIIYLCSNQEFKKAFQSLL-GVHCLRMTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPMH PGNTTVSEDEALESETHFALELLKFSREKKAAKTLGIVVGCFVLCWLP--FFLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAIFSAVGSFYLPLAIILAMYCPVYVVÄQKE-----SPGLKEGQKIEKSDSEQVI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTILSVVSFIVIPLIVMIACYSVVFCAAPPQHALLYNVKPHSLEVFVKDCVENEDEEGAE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109;
                                                                                                                                                                                                                                      1-422 <FUJ>
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NID. 3202540; PIDW AAA40612.1; PTD 3202541
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                                                                                                                                                and mRNA tissue distribution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 477
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                                                                                                                                             rat 5-hydrd
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A.Cross-references. GB.M76446; NID:g177806; PIDN:AAA35496 1; I A;Experimental source: hippocampus C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane protein F;56-79/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bruno, J.F.; Whittaker, J.; Song, J.; Berelowitz, M. Biochem. Biophys. Res. Commun. 179, 1495-1490, 1991
A;Title: Molecular cloning and sequencing of a cDNA encoding A;Reference number. JH0447; MJID:92028892; FMID:1656955
A;Accession: JH0447
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C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen
F;37-62/Domain: transmembrane #status predicted <TM1>
F;74-98/Domain: transmembrane #status predicted <TM2>
F;109-134/Domain: transmembrane #status predicted <TM3>
F;109-134/Domain: transmembrane #status predicted <TM5>
F;153-178/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-501 < BRU >
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                                                                                                     F;339-363/Domain: transmembrane #status predicted <TM7>
                                                                                                                                   F;308-331/Domain· transmembrane #status
                                                                                                                                                   F;210-233/Domain: transmembrane
                                                                                                                                                                                F;172-196/Domain: transmembrane
                                                                                                                                                                                                        F;128-151/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                 F;93-116/Domain: transmembrane #status predicted <TM2>
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        Matches
                             Query Match
Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 ISLAHGIIRSTVLVIFLAASEVGN--IVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VITIIIWLFFLCCCIHPYVYGYMHKTIKKEIQDMLKKFFCK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDWPPCAENRAVGTPCTNGAVRQGDDEATLEVIEVHRVGNSKEHLPLPSESGSNSYAPAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGAIINWLGYSNSLLNPVIYAYFNKDFQNAFKKIIKCKFCR 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LERKMERNAEAKRYMALARERKTVKTLGIIMGTFILCWLPFFIVALVLPFCENSCHMPAL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLLLMLVLYGRIFPAAR-----FRIRKTVPKVEKFGAGTSLGTSSAPPPKKSLNGQPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLIVMIACYSVVFCAAFPQHALLYNVKFHSLEVPVKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPRRAMALISLTWLIGFLISIPPMLGWRTP--EDRSDPDACTISKDHGYTIYSTEGAEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLPMAALYQVLNKWTLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDPIDYVNKR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPPGYLLLYGTWIVAILOSTPPLYGWGQAAFDERNALCSMIWGASPSYTILSVVSFIVI
96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98;
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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     Conservative
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                             15.6%;
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6; Pred. No. 2.5e-20;
69; Mismatches 163; Indels
58;
                                                                                                                                                      #status predicted <TM4>
#status predicted <TM5>
                                                     Score 326.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - DEEGNEKKEEFODEMIJFESTE PSEENSNSNSPF-
     Pred. No. 8e-
8; Mismatches
                                                                                                                                predicted <TM6>
                                8e-20;
                                                     DB 2;
157;
                                                     Length 501;
        Indels
                                                                                                                                                                                                                                                                                                                                                                 PID-g177807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a human alpha 1A adrenergic
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        10;
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29 ANGIIRSTVLVIFLAASEVGNIVMALVMOREFPOMAQVTNRFIFNLLVTDLLQISLVAPWV 88

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                                                                                                                                                                                                                                                                                                                   F;89-123/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: GDB:ADRA1A; ADRA1R
A;Cross-references: GDB:118749; OMIM:104219
A;Map position: 20pter-20qter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references GB:D29952; NID:g914933; PIDN:BAA06222.1; PID:g914934
R;Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A;Title: Cloning, expression and characterization of human alpha adrenergic receptors al
A;Reference number: JC2331; MUID:94296402; PMID:8024574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-1A-adrenergic receptor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 13-Aug-1999
C;Accession: I39369; UC231
R;Esbenshade, T.A.; Hirasawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Minneman, K.P.;
Mol. Pharmacol. 47, 977-985, 1995
A;Title: Cloning of the human alpha 1d-adrenergic receptor and inducible expression of A;Reference number: I39369; MUID:95265059; PMID:7746284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-30,'G',32-521,'P',523-572 <WEI>
A;Note: the authors translated the codon CCC for residue 522 as Arg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residues: 1-572 <RES>
89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
                                                                                 94 AQĞVGVGVFLAAFILMAVAĞNLLVILSVACNRHLQTVTNYFIVNLAVADLLLSATVLFFS 153
                                                                                                                                 29 AHGIIRSTVĻVIFLAASFVĢNIVLAĻVLQRKPQĻLQVŢŅRFĮFNĻĻVŢDĻĻQISLVAPWV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 LFPQLKPSEGVFKVİFWLGYFNSCVNPLIYPCSSREFKRAFLRLLR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 VDVETQVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 EFQDEMNIPESCPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVW 314
                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 TFRSSLSV-RLLKFSREK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 IVVMYCRVYVVARSTTRSLEAGVKRERGKASEVVLRIHCRGAATGAD--GAHGMRSAKGH 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 MIACYSVVFCAAR-RQHALLYNVKRHS-----LEVRVKDCVENEDEEGAE-----KKE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 AAILALLWVVALVVSVGPLLGWKEPVPPDER--FCGITEEA--GYAVFSSVCSFYLPMAV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 YLLLYGTWIVAILQSTPPLYGWCQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 ATMEVLGÉWAFGRAFCDVWAAVDVLCCTASILSLCTISVDRÝVGVRHSLKÝPAIMTERKA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 VATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRG 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37/3
                                                                                                                                                                                    h 15.6%; Score 326.5; DB 2; Length Similarity 27.7%; Pred. No. 9.3e-20; 96; Conservative 58; Mismatches 157; Indels
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                                                                                                                                                                                                                                                                                                (covalent) #status predicted
                                                                                                                                                                                                                                             DB 2; Length 572;
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C;Keywords: G protein-coupled receptor; transmembrane protein
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Gene 131, 243-247, 1993

A;Title: Isolation and characterization of the gene encoding the rat alpha 1B adrengergic A;Reference number: JC1525; MUID:94010315; PMID:8406017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Pesidues: 1-202'C',204-206,'C',208-305,'C',307-414,'QK',417-439,'C',441-483,'ATA',487-
A;Cross-references: EMBL:X51585; NID:g55557; PIDN:CAA35934.1; PID:g55558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Voigt, M.M.; Kispert, J.; Chin, H. Nucleic Acids Res. 18, 1053, 1990
A;Title: Sequence of a rat brain cDNA encoding an alpha-1B adrenergic receptor.
A:Reference number: S08400; MUID:90192094; PMID:2156222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 317/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L08610; NID:g202624; PIDN:AAA40647.1; PID:g202626
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A; Residues: 1-515 <GAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-1B-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999
C;Accession: JC1525; S08400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: translation not shown
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306 CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDML 359
                                                                                     263 DTLSSTKAKGHNPRSSIAVKLFKFSREK------KAAKTLGIVVGMFILSWLPF 310
                                                                                                                                                                                                                                                                 194 ILSVVSFIVIPLIVMIACYSVVFCAARRQHALL------YNVKRHSLEVRVKDCVENE 245
                                                                                                                                                                                                       205 LFŚSLGSFYIPLAVILVMYCRVYIVAKRTTKNIEAGVMKEMSNSKELTĽRIHSKNF--HE 262
                                                                                                                                                                                                                                                                                                                          148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204
                                                                                                                                                                                                                                                                                                                                                                                   134 IHPLSYPSKMTORRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                            88 AIADLLLSFTVLÞFSATLEVLGYMVLGRIFCDIWAAVDVLCCTÁSILSLCAISIDRÝIGV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 LFPOLKPSEGVFKVIFWLGYFNSCVNPLIYPCSSREFKRAFLRLLR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 ŚŚNSTLPQLDVTRAISVĠL----VLGAFILFAIVĠNILVILSVACNRHLRTPTNYFIVNL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 SSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 VDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 TFRSSLSV-RLLKFSREK------KAAKTLAIVVGVFVLCWFPFFFVLPLGS- 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 EFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAVLAVW 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 MIACYSVVFCAAR-ROHALLYNVKRHS-----LEVRVKDCVENEDEEGAE-----KKE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AAILALLWVVALVVSVGPLLGWKEPVPPDER--FCGITEEA--GYAVFSSVCSFYLPMAV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 ATMEVLGFWAFGRAFCDVWAAVDVLCCTASILSLCTISVDRYVGVRHSLKYPAIMTERKA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                              DEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.5%; Score 324; DB 2; 26.3%; Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70; Mismatches 161; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 515;
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A;Genetics:

A;Genetics:
A;Gene: GDB:HTPlA; ADPEDPLI; APPEPLI
A;Cross - references: GDB:1206A6; QMIM:100760

A;Map position: Scen-5ql1
A;Cross - references: Gpr:1206A6; QMIM:100760
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C;Superfamily: vertebrate #status predicted <IM1>
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E;110-122/Domain: transmembrane #status predicted <IM4>
E;110-122/Domain: transmembrane #status predicted <IM4>
E;110-122/Domain: transmembrane #status predict
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A;Residues: 1-9 < APAR>
A;Cross references. EMBL.Z11168, HID:g1033027, FIDN:CAA77560.1; FID:g1033028
A;Cross references. EMBL.Z11168, HID:g1033027, FIDN:CAA77560.1; FID:g1033028
A;Cross references. EMBL.Z11168, HID:g1033027, FIDN:CAA77560.1; FID:g1033028
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A;Cross references: EMBL.X13556; HID:g35523, FIDN:CAA31908.1, FID:g35524
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A;Cross references: EMBL.X13556; HID:g35523, FIDN:CAA31908.1, FID:g35524
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A.A.Coession: ISA176

A.A.SCLATUS: Preliminary; translated from GB/EMBL/DDBJ

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: mPNA

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A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

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A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

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A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mPNA

A.B.Coession: Type: mP
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F;379-403/Domain: transmembrane #status predicted <TM7>
F;10,11,24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;109-197/Disulfide bonds: #status predicted
F;420/Binding site: palmitate (Cys) (covalent) #status predicted
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A,Accession: 138209
A,Status; preliminary; translated from GB/EMBL/DDBJ
A,Molecule type DMA
A,Residues: 1 422 c7AC>
A,Residues: 1 422 c7AC>
A,Cressiones EMBL X57809, NIC-316429, PIDN CAA40362.1; PID:316429
R;Parks, C.L.; Chang, L.S.; Shenk, T
Rucloic Acids Ros. 19, 7155 7169, 1991
A,Title: A polymorase chain reaction mediated by a single primer, cloning of genomic seq
A,Reference number: 137104, MUID:92115564; PMID:1766875
A,Recession: 137104
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Mutat. Bes. 179, 89-101, 1987
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N;Alternate names: 5-hydroxytryptamine receptor 1A (5-HTR1A)
C;?peries H-mo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title: DNA replication-blocking properties of adducts formed by aflatoxin B1-2,3-dich: Reference number T38200; MUID:87258013, PMID:3110609
                                                                                               84 VAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSIIHPLSYPSKM 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                     31 VTVSYQVITSLLLGTLIFCAVLGNACVVAAIALEP--SLQNVANYLIGSLAVTDLMVSVL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 ISLAHGIIPSTVLVIFLAASEVGN -- IVLALVLQEKELLLQVTNRFIENLLVTDLLQISL 83
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Similarity 24 0%; Pre
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A.Molecule type: meNA
A.Besidues: 336-176 /7,178-241, L',243-246,/V',248 260,/W',264-303,/H',305 309,/I',331-3
A.Besidues: 336-176 /7,178-241, L',243-246,/V',248 260,/W',264-303,/H',305 309,/I',331-3
A.Besidues: 336-120339
A.Gross-references: GB.L20339
C.Soperfamily: vertebrate rhodopsin
C.Koywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen
F.37-62/Domain: transmembrane #status predicted <TM1>
F.74-98/Domain: transmembrane #status predicted <TM2>
F.110-132/Domain: transmembrane #status predicted <TM3>
F.153-178/Domain: transmembrane #status predicted <TM4>
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F.153-178/Domain: transmembrane #status predicted <TM4>
F.153-178/Domain: transmembrane #status predict
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P:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I., O
Genomics 18, 175-184, 1993
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H/Alternate names: 5-bydroxytryptamine receptor 1A (5-HTRIA)
C/Species: Mus musculus (house mouse)
C/Date. 02-Jul-1996 #sequence_revision 02 Jul-1996 #text_change 13 Aug-1999
C/Accession: 149375, A57508
C/Accession: 149375, A57508
C/Accession: 149375, A57508
C/Accession: 13, 5164-5171, 1993
J. Neurosci. 13, 5164-5171, 1993
A/Title: Cloning and differentiation_induced_expression of a murine serotoninlA receptor
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A;Reference number: A48909, MUID:94116990; FMID:8288218
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C;Accession A45121;
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
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A;Title: Molecular cloning and expression of the cDNA for the hamster alpha-1-adrenergic A;Reference number: A40491; MUID:89017157; PMID:2845398
A;Accession: A40491
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
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;Species: Homo sapiens (man)
;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Apr-2000
;Accession: A45121; JC2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-515 < COT>
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                                                                                                                                                                                                311 -FIALPLGSLFSTLKPPDAVFKVVFWLGYFNSCLNPIIYPCSSKEFKRAFMRIL 363
                                                                                                                                                                                                                                              306 CFLAVLAVWVDVBTQVPQWVITIIIWLFFLQCÇIHPYVYGYMHKTIKKBIQDML 359
                                                                                                                                                                                                                                                                                                 263 DTLSSTKAKGHNPRSSTAVKLFKFSREK------KÅÅKTLGIVVGMFILCWLPF 310
                                                                                                                                                                                                                                                                                                                                                                                                 205 LFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF--HE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                               194 ILSVVSFIVIPLIVMIACYSVVFCAARROHALL-----YNVKRHSLEVRVKDCVENE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 IHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 SSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNL 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                              DEEGAEKKEEFQDEMNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIADLLLSFTVLPFSATLEVLGYWVLGRIFCDIWAAVDVLCCTASILSLCAISIDRYIGV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSVDRYLSI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSNSTLPQLDVTRAISVGL----VLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKBIQDMLKKFFCK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PACLERKNERTAEAKRKMALARERKTVKTLGIINGTFILCWLPFFIVALVLPFCESSCHM 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --DCVENEDE-----EGAEKKEEFQDEMNIPE----SLP-PSRRNSNSNPPL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPLLLMLVLYGRIFRAAR-----FRIRKTVKKVEKKGAGTSFGTSSAPPPKKSLNGQPG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPRRAAALISLTWLIGFLISIPPMLGW-RAPEDRSNPNECTI--SKDHGYTIYSTFGAFY 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 162; Indels 30; Gaps
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alpha-1A adrenergic receptor - rat C;Species: Rattus norvegicus (Norway rat)
C;Becies: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Apr-2000
C;Accession: A38731; A53280
R;Lomasney, J.W.; Cotecchia, S.; Lorenz, W.; Leung, W.Y.; Schwinn, D.A.; Yang-Feng, T.L.;
J. Biol. Chem. 266, 6365-3369, 1991
A;Title: Molecular cloning and expression of the cDNA for the alpha-1A-adrenergic receptors, Reference number: A38731; MUID:91177889; PMID:1706716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;203-227/Domain: transmembrane #status predicted <TM5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 5q31.1-5q33.2
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
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A;Note: sequence extracted from NCBI backbone (NCBIP:116785)
A;Note: this translation is not annotated in GenBank entry HUMADRENB, release 113.0 #date R;Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.; Eliochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A;Title: Cloning, expression and characterization of human alpha adrenergic receptors alpha A;Reference number: JC2331; MUID:94296402; PMID:8024574
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A;Residues: 1-158,'p',160-244,'H',246-314,'F',316-380,382-517 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Ramarao, C.S.; Denker, J.M.; Perez, D.M.; Gaivin, R.J.; Riek, R.P.; Graham, R.M. J. Biol. Chem. 267, 21936-21945, 1992
A;Title: Genomic organization and expression of the human alpha 1B-adrenergic receptor. A;Reference number: A45121; MUID:93016158; PMID:1328250
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                                                                                                                                                                                                                                                                                                                                                                                                                                311 -FIALPLGSLFSTLKPPDAVFKVVFWLGYFNSCLNPIIYPCSSKEFKR 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 CFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 DTLSSTKAKGHNPRSSIAVKLFKFSREK------KAAKTLGIVVGMFILCWLPF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 LFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF--HE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 ILSVVSFIVIPLIVMIACYSVVFCAARRQHALL----YNVKRHSLEVRVKDCVENE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 RYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPND-DKECGVT--EEPFYA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 IHPLSYPSKMTORRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 AMADLLLSFTVLÞFSAÁLEVLGYMVLGRIFCDIWAAVDVLCCTÁSILSLCAISIDRÝIGV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 SSNSTLP----QLDITRAISVGLVLGAFILFAIVGNILVILSVACNRHLRTPTNYFIVNL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 SSHTCMPLSKMPISLAHGIIRSTYLVIFLAASFYGNIVLALVLQRKPQLLQVTNRFIFNL 73
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A; Molecule type: mRNA

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UNOTE: sequence extracted from NCBI backbone (NCBIP:73541)
Superfamily: vertebrate rhodopsin
UNEYWORDS: 3 protein coupled receptor; glycoprotein; transmembrane protein
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Molecule type: mRNA; Accession: Ac.'F', 38:58', 'I', 60 202, 'I', 204-305, 'R', 307-366, 'I', 368-370, 'I', 372-559 <F
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                                                                                                                                                                                                                                                            312 YPGTCSSKCHTLESSLSVPILLESSERKAAKTIAIVVGVFVICWEPEFFVIDIGS-LFPC 370
371 LKPSEGVEKVÍFMÍGYENSÁVNÁLTÝÞÁSSÞEFKÞAFLÞLÍÞ 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 IVVMYCPVYVVARS-----TTPS1.EAGIF----PEPGFASEVVI.BIHCPGAATSAFG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 MINCYSVVECANFEGHALLYMVKFHSLEVEVKKKCVENEDEBGAE KKEEFQDEMMIFES 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AATTALLWAVALVVSVGPLLGWKEPVPPDER--FCGIT--EEVGYAIFSSVCSFYLPMAV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 YLLLYGTWIVAILQSTPPLYGWGQ-AAFDERNALCSMIWGASPSYTILSVYSFIVIPLIV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 ATMEVLGEWAFGRTFCDVWAAVDVLCCTÄSILSLCTISVDRYVGVRHSLKYPAIMTERKA 207
                                                                                                                              319 ТОМРОМУІТІІНШЕВЬООСІНРУМУВУМНКТІККЕІОВЫК 360
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Local Similarity 27 5%; Pred No 9.4e-19;
hes 94; Conservative 59; Mismatches 162; Indels 27; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 AHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RR AQGVGVGVFLAAFILTAVAGNLLVILSVACNEHLQTVTNYFIVNLAVADLLLSAAVLPFS 147
                                                                                                                                                                                                                                                                                                                                                                                                 ENSWENEFIPECYQCEAAKVIFIIIESYVLSLGPYCFLAVLAVWVDVE 318
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cearch completed: February 11, 2003, 11:10:40 Job time : 23 secs